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A BIOMETRICAL-GENETIC ANALYSIS OF SOME QUANTITATIVE CHARACTERS IN A FIVE-PARENT DIALLEL CROSS OF COMMON WHEAT (*TRITICUM AESTIVUM* L.)

by

© BARKAT ALI SOOMRO

A THESIS

SUBMITTED TO THE FACULTY OF GRADUATE STUDIES AND RESEARCH

IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE

OF DOCTOR OF PHILOSOPHY

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The undersigned certify that they have read, and recommend to the Faculty of Graduate Studies and Research for acceptance, a thesis entitled A Biometrical-Genetic Analysis of Some Quantitative Characters in a Five-Parent Diallel Cross of Common Wheat (*Triticum aestivum* L.) submitted by Barkat Ali Soomro in partial fulfilment of the requirements for the degree of Doctor of Philosophy.

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Date January 14, 1974

To Mämtaaz Khàtoon Soomro.

ABSTRACT

Common wheat (*Triticum aestivum L.*) cultivars Marquis, Chinook, Khush-hal, Ciano-67 and Inia-66 were used as parents of a five-parent diallel cross. The F_1, F_2, backcross and selfed backcross generations of this diallel cross were used as materials in this study. The experimental data were investigated by means of principal factor analysis, general and specific combining ability analysis, diallel cross analysis for genetic components of variation and genotype-environment interaction analysis. The data on ten characters were recorded from materials grown at Ellerslie and Parkland. The characters considered were: onset-of-heading, final heading, heading-span, plant height, number of tillers per plant, number of spikelets per spike, number of seeds per spike, weight of seeds per spike, 1000-kernel weight and yield per plant.

In the factor analyses, correlation matrices indicated that early maturing varieties were high yielding. Yield per plant was positively correlated with its subcharacters or components. There was no correlation between yield and plant height. Varimax rotated factor matrices for each generation of the diallel cross constituted five principal factors which were named according to the magnitude of the factor loading on the characters. The results of the factor analyses confirmed the conclusions drawn from correlation analyses. The scores of factor loadings on various characters were different for two locations but the generations appeared not to affect them significantly.

The general and specific combining ability analyses indicated that parental lines possessing high GCA's usually produced hybrids with low SCA's and therefore general combining ability of the parents does not necessarily constitute a criterion for evolving hybrids with high specific combining ability. The variances for GCA's were usually greater than those for SCA's for all the characters, and in those cases where SCA-variances were larger, the importance of non-additive gene effects for the characters concerned has been emphasized. SCA-variances significantly higher than GCA variances indicated instabilities of the cultivar for the character concerned and therefore these differences may be used as criteria for the selection in pedigree-record breeding. Mean squares for GCA's were in general all significant. Analysis also showed that GCA's were not significantly affected either by generations of the diallel set or by locations. The stability of the response of each cultivar with respect to its GCA was consistent over two locations.

The mean degree of dominance with respect to different characters ranged from partial to over-dominance. The proportions of alleles with positive and negative effects were not the same for all the characters: complete symmetry was observed for some and asymmetry for others. For some characters dominant and recessive genes in the parents were in equal proportions and for others either there was a preponderance of dominants or of recessives. Character differences were found to be controlled by at least one to three groups of genes. The analyses for the characters considered have shown that

the genetic components of variation were relatively stable over the generations. They were more consistent when estimated from the variances and covariances of adjusted treatment means (from *ANOVA* of partially balanced lattice design) than when estimated from unadjusted means (experiments treated as randomized blocks).

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INTRODUCTION

The degree to which a quantitative or metrical trait is phenotypically expressed in individuals depends on their genotype and the environmental conditions under which they are grown. It is assumed, and the experimental data seems to confirm it in most of the cases, that the genotype considered with respect to a metrical character is a set of genes referred to by Mather individually as polygenes and collectively as a polygenic system (Mather, 1949). These genes are often inter-dependent both in their action and transmission. In a polygenic system underlying a quantitative character, the allelic and non-allelic interactions are the most usual forms of manifestation of gene effects and inheritance pattern. The interaction of alleles at a given locus is known as dominance, while non-allelic interaction, viz., interaction between the genes at different loci, may take the form of complementary-gene, duplicate-gene or other classical relationships. All these effects are referred to generally as 'epistasis' in biometrical genetics.

Different genotypes defined with reference to a metrical character do not react alike to a given change in environment. This means that genotype and environment are not independent in their action in producing the phenotype. Consequently the variation in the degree of expression of the character is assumed to consist of genotypic, environmental and genotype-environment interaction components which may respectively be partitioned in a biometrically defined experimental design. The measurement of genotype-environment interaction in the diallel cross

is quite efficient and informative, since a number of parental strains can be assessed together with their hybrid generations.

The diallel cross technique is one of the conventional approaches used in biometrical genetics to obtain adequate information regarding the inheritance of a quantitative character. The procedure, first introduced by Schmidt (1919) involves crossing a set of parental lines in all possible combinations, including their reciprocals, in order to obtain an estimation of the magnitude of genetic variability ascribable to the differences among the parental lines. The quantitative genetic analysis of a diallel cross based on a set of postulated assumptions is presented and discussed in detail by Jinks and Hayman (1953), Hayman (1954a, 1954b, 1958 and 1960), Jinks (1954 and 1956) and Kempthorne (1956). By means of pertinent parameters obtainable from the analysis of the diallel cross, the mean degree of dominance, the proportion of positive to negative alleles at loci exhibiting dominance, the proportion of dominant to recessive genes in the parents, and the correlation between the parental order of dominance and parental measurements can be determined. In addition, the graphical analysis of the regression of array covariances (W_r) on array variances (V_r) permits the separation of true dominance from the spurious one caused by non-allelic interaction and categorizes the parents according to their degree of dominance.

The analysis of genotype-environment interaction by means of a diallel cross replicated in time, in space or in both time and space, provides information on the pattern of reaction of homozygous parents and their hybrids to environmental variation. The value of such an analysis

is that the significant inter-environmental differences characteristic of different genotypes are reflected in the array variances and covariances by their effects on the relative magnitude of components of these statistics. The project reported in this thesis deals with this type of analysis of genotype-environment interaction in a five-parent diallel cross in common wheat (*Triticum aestivum* L.). The purpose of the investigation was to obtain information regarding the extent to which the genetic components of variation and the combining abilities of the parental lines are affected by environmental changes.

REVIEW OF LITERATURE

General background

A diallel cross involves the mating of n genotypes, individual clones or homozygous lines in all possible combinations to give $[n(n-1)]$ crosses, including reciprocals. The total number of such combinations comes to n^2 if the parents are also included as selfs. The n^2 combinations may be arranged in the form of a square matrix, the rows and columns of which correspond to the offspring of each parent, the n parents themselves occupying the main diagonal. Such an arrangement of arrays, known as a diallel table, may be complete or incomplete. Complete tables consist of all n^2 entries, while in incomplete ones the parental or reciprocal entries may be absent. Griffing (1956) has developed four possible methods of constructing a diallel table, together with the corresponding forms of analysis. These are: (1) the parents, all the F_1's and their reciprocals are included (n^2 combinations); (2) the parents and one set of F_1's are included but not the reciprocals [$\frac{1}{2}n(n+1)$ combinations]; (3) one set of F_1's and reciprocals are included but parents are not [$n(n-1)$ combinations]; and (4) one set of F_1's is included but the reciprocal crosses and the parents are not [$\frac{1}{2}n(n-1)$ combinations]. For each of these combinations, Griffing has developed two kinds of statistical analyses, arising from different assumptions regarding the sampling nature of the experimental material; either it is assumed to be a random sample from the population or it is assumed to be deliberately chosen, and therefore not a random sample.

The biometrical-genetic analysis of a diallel cross as formulated by Hayman (1954b) is based on the following set of assumptions:

1. Homozygous parents
2. Normal diploid segregation
3. No differences between reciprocal crosses
4. Independent action of non-allelic genes
5. No multiple allelism
6. Genes independently distributed between the parents.

The genetic analysis, discussed by different authors (Hull 1945; Hayman 1954a, 1954b, 1958, 1960; Jinks 1954, 1956 and Jinks and Hayman 1953) implies the estimation of genetic components of variation from the following second degree statistics:

V_{OLO} = Variance of the parents

W_r = Covariance between the parents and their offspring in one array (rth array)

W_{OLO1} = Mean covariance between the parents and their offspring over the arrays

V_r = Variance of the rth array

V_{1L1} = Mean variance of the arrays

$(M_{L1}-M_{LO})$ = Difference between the mean of the parents and the mean of their n^2 progeny

The description of the genetic components of variation is given below:

D = Component of variation due to additive gene effects

H_1 = Component of variation due to dominance effects of the genes

H_2 = Component of variation due to dominance effects, corrected for gene distribution

F = Covariation between additive and dominance effects over all the arrays. Thus F could be used to determine the relative proportion of dominant to recessive alleles in the parents involved.

The expected values of these genetic components of variation in terms of variances and covariances have been described by Mather (1949), Hayman (1954b, 1958), Jinks (1954, 1956) and Mather and Jinks (1971).

The relationship between the array variances and covariances, expressed graphically, shows the overall genetic situation with respect to the inheritance-pattern of a particular character. When the set of assumptions described earlier are valid, the W_r-V_r differences are constant over the arrays, the regression of covariance on the array variance is a straight line of unit slope and all the points of W_r, V_r intercepts lie on this line. The upper and the lower limits where the W_r, V_r intercepts can lie are the points where the regression line intersects the limiting parabola. These points correspond respectively to the completely recessive and completely dominant parents, and thus show the possible limits of selection.

A deviation from the expected regression line of unit slope indicates the presence of non-allelic interaction. Any type of non-allelic interaction affecting the crosses in an array will inflate the variance of that array and reduce the parent-offspring covariance. Such an increase in variance relative to covariance will move the W_r, V_r graph towards the right, giving an apparent increase in dominance, and will cause the slope of the regression line to be less than unity. Thus, with $H_1 = D$ (complete dominance), $V_{1L1} + W_{0L01} = 1$ and the line of unit

slope will pass through the origin; with $H_1 > D$ (over-dominance), $V_{1L1} \div W_{0L01} > 1$ and the line will cross the ordinate below the origin; and with $H_1 < D$ (partial dominance), $V_{1L1} \div W_{0L01} < 1$ and the regression line will pass above the origin. If, of course, $H_1 = 0$ there is no regression. The mean degree of dominance is measured by $(H_1 \div D)^{1/2}$. The ratio $(H_2 \div 4H_1)$ provides an estimate of the proportion of genes with positive and negative effects in the parents. The proportion of dominant to recessive genes in the parents is given by $[(4DH_1)^{1/2}+F] \div [(4DH_1)^{1/2}-F]$ and the number of groups of genes controlling the character and showing dominance can be determined by the formula $[h^2/H_2]$.

The failure of any one of the six postulated assumptions invalidates the analysis to a certain extent. The effects of the failure of these assumptions are discussed by Hayman (1954b). The methods of analysis of complete diallel tables as developed by Yates (1947), Hayman (1954a), Durrant (1965) and Jinks *et al* (1972) allow, among others, for the detection and testing of 'reciprocal differences'. Significance of the c pertaining to reciprocal differences in Hayman's analysis implies the expectation of two values for each of the genetic components of variation, D, H_1, H_2 and F from the diallel table; one from the use of column arrays and the other from the use of row arrays. This ambiguity may be removed by replacing the off-diagonal cells of the diallel table by the common mean for the cross and its reciprocal. However, with significant c, the errors of the parameters will be inflated. Departure from independent action of non-allelic genes may be checked by examining

the $W_r - V_r$ values for homogeneity. Heterogeneity of $W_r - V_r$ differences indicates failure of the assumptions postulated. If this is the case, the inspection of the V_r, W_r graph would show which of the arrays contribute mostly to this failure. The disparate arrays may be eliminated, leaving a sub-diallel table for analysis that satisfies the null hypothesis. The results of the analysis would be valid, of course, for the remaining arrays.

Manifestations of 'non-allelic interaction', 'multiple allelism' and 'correlated gene distribution' introduce serious complications into the diallel analysis. They disturb the direction and mean degree of dominance, inflate the estimated proportion of dominant to recessive genes in the parents and reduce the estimate of the number of genes controlling a particular character. A test of homogeneity of variances of $W_r - V_r$ values has been advocated as an appropriate method for their detection.

Application of diallel cross analysis

The literature pertinent to diallel cross analysis as applied to plant breeding programmes is fairly impressive. In non-cereal crop plants, the technique has been widely used in the study of various quantitative characters. Thus this technique has been applied to bromegrass (Knowles 1950; Greesom and Kalton 1956; Neilson and Kalton 1959; Dunn and Wright 1970), alfalfa (Kehr 1961; Theurer and Elling 1963a, b; Wilcox and Wilsie 1964), flax (Carnahan 1947; Durrant and Tyson 1964; Murty *et al* 1967; Anand and Murty 1968, 1969), cotton (Turner 1953; Marani 1963;

White and Richmond 1963; Marani 1964; Miller and Marani 1963; White and Kohel 1964), tobacco (Jinks 1954, 1956; Matzinger *et al* 1962; Marani and Sachs 1966; Povilaitis 1966; Legg *et al* 1970; Povilaitis 1970), strawberry (Morrow *et al* 1958; Aalders and Craig 1968; Watkins and Spangello 1968; Spangello *et al* 1971) and *brassica* (Johnston 1968a, b; Chiang 1969).

In cereals, a considerable number of studies using diallel analysis have been made with rice (Mohammad and Hanna 1965; Athwal and Singh 1966a, b; Wu 1968a, b; Cheng and Chang 1970), maize (Kinman and Sprague 1945; Sprague and Federer 1951; Bauman 1959; Matzinger *et al* 1959; Sprague 1964; Troyer and Hallauer 1968; Eberhart and Russell 1969; Poneilet and Bauman 1970), barley (Johnson and Aksel 1959; Aksel and Johnson 1961; Eunis *et al* 1962; Fasoulas and Allard 1962; Aksel and Johnson 1963; Johnson and Aksel 1964; Norington 1967, 1968; Persson 1969; Yap and Harvey 1971; Riggs and Hayter 1972, 1973) and *sorghum* (Chiang and Smith 1967a, b; Liang 1967; Liang *et al* 1968).

In wheat, the first report on the use of diallel analysis is that of Whitehouse and co-workers (1958). Of the five characters studied by them in a 4 x 4 diallel cross, viz., single kernel weight, grains per spikelet, spikelets per spike, ears per plant and yield per plant, all except yield per plant were found to be under additive genic control. For total yield, a generalized type of gene action was found in the F_1 but the F_2 generation exhibited a localized multiplicative type of gene action.

Lupton (1961) performed a diallel analysis of the yield of winter wheats. Though there was no non-allelic interaction (as revealed

by W_r, V_r graphs) in either the drilled or space-planted experiments, the position of the parents with respect to dominance was significantly changed in the two environments. The highest yielding parent, Capelle, exhibited dominance in the space-seeded trial and was reported to be the most recessive in the drilled trial. This change in yield inheritance was attributed to environmental differences of the inter-plant competition type which appeared to affect drill plantings more than space-seedings. In a later study (Lupton 1965), an incomplete diallel system, where reciprocals were excluded, was used to study the yield of spring wheat varieties replicated both in space and time, for F_1, F_2 and F_3 generations. In all cases, interaction of over-dominance with site was highly significant, establishing consistency in the performance of the parents and their hybrid combinations.

Crumpacker and Allard (1962) analysed heading date in ten spring wheat varieties in a complete diallel test, replicated over three years. The results indicated substantial differences among the parents, generally categorized as highly dominant, moderately dominant, moderately recessive and highly recessive. The genetic system governing the maturation time of the parents, F_1's and F_2-generation hybrids consisted of a very few major genes showing dominance and was reported to be operating consistently in different years.

Fonseca (1965) studied the inheritance of yield and yield-components in a seven-parent diallel cross of wheat. The author reported significant differences among the parental lines used. The

graphical analysis revealed partial dominance to slight over-dominance for all the characters studied. Since all the F_1's yielded higher than either of their respective parents, the author proposed a new term, heterobeltiosis, to describe the better performance of the F_1 over the better parent in the cross.

Bagnara (1967) performed a diallel analysis on normal and radiation-induced mutant lines of durum wheat. The results revealed significant differences between the lines and the mutants derived from them with regard to the expression of the degree of dominance. All the characters under study except spikelets per spike exhibited partial dominance.

Fonseca and Patterson (1968) studied hybrid vigour in a seven-parent wheat diallel to determine the diversity of germ-plasms in hill-planting experiments. The authors reported significant heterobeltiosis for yield and kernel-weight in half of the F_1 hybrids. The yield and kernel-weight estimates, were respectively 100% and 101 to 115% greater than either parent in hilled as against experimental nursery plots.

Walton (1969) studied the association of several morphological characters with yield in a seven-parent spring wheat diallel. He reported that the distance of the spike above the leaf-sheath at maturity and flag-leaf area were directly proportional to yield, and that yield, flag-leaf area and spike length were partially dominant.

Paroda and Joshi (1970) performed a genetic analysis of a complete 6 x 6 wheat diallel test for yield and its principal components: 1000-kernel weight, kernels per spike and tillers per plant. Yield and

1000-kernel weight exhibited non-allelic interaction of the duplicate-gene and complementary-gene type, respectively. For both characters, the variances for additive gene effects were significant.

Hsu and Walton (1970) studied gene action for yield and its components (spikes per plant, spikelets per spike, kernels per spike and 1000-kernel weight) in a 5 x 5 wheat diallel. For all the characters studied, the genetic variation was reported to be due to additive and dominance gene effects. Yield per plant exhibited complete, and its components partial, dominance.

Bitzer *et al* (1971) reported gene action and hybrid vigour in a six-parent wheat diallel. The results of two years of study revealed that the yield of the F_1 hybrids was not significantly higher than that of the parental strains. However, according to the graphical analysis of regression of W_r on V_r, plant height, kernel weight and spikelets per spike exhibited partial dominance while yield per plant showed over-dominance.

Kaltsikes and Lee (1971) estimated the genetic parameters for degree of dominance, ratio of total number of dominant to recessive parental genes and heritability for yield and its components in a 6 x 6 diallel of durum wheat. The average degree of dominance ranged from in-complete dominance to over-dominance and an excess of dominant over recessive alleles in the parents was found for all the characters studied. Since the heritability estimates for yield were as high as 61%, the authors suggested a pedigree selection procedure in breeding for yield characters in durum wheat.

General and specific combining ability

In quantitative genetics two types of combining ability, viz., general combining ability and specific combining ability are considered. General combining ability (GCA) refers to the average performance of a parental line as reflected in its hybrid combinations, while specific combining ability (SCA) refers to the performance of a particular cross. According to Sprague and Tatum (1942), GCA is due to genes which are largely additive, and SCA to genes showing non-additive effects. Nakamura (1956) considers GCA as 'an index of the number of effective genes' and SCA as 'an index of the number of common genes and the interaction between their alleles'. According to Fryxel *et al* (1958), GCA is the ability of a parental strain to produce promising or non-promising genotypes in its hybrids, regardless of the other parent involved, while SCA refers to this ability in hybrid combinations with certain other parental strains.

In a detailed examination of combining ability in the diallel cross, by Griffing (1956), eight procedures of statistical analysis have been proposed. These have been developed for four different diallel crossing schemes and for two alternative assumptions regarding sampling nature.

Kronstad and Foote (1964) using Griffing's diallel analysis for estimating GCA and SCA effects in ten winter wheat varieties found that a large portion of the total genetic variation for yield and yield components was associated with significant GCA effects. SCA effects were significant for yield per plant and plant height but not for yield components.

Fonseca (1965) studied the performance of F_1 hybrids for yield and yield components in a 7 x 7 diallel cross using Griffing's method 4 (one set of F_1's is included in the diallel table but the reciprocal crosses and the parents are not) with fixed model. The results revealed that all the mean squares for GCA and some of the mean squares for SCA were significant.

Brown *et al* (1966) found that most of the variation in yield and other characters among F_1 wheat hybrids was associated with high GCA rather than with SCA variances.

Singh *et al* (1969) in an analysis of a 7 x 7 wheat diallel for combining ability and genetic parameters for yield and its components, reported importance of additive gene effects for general over the non-additive ones of specific combining ability for yield components. The variances for GCA and SCA in the case of yield were of the same order of magnitude, implying additive as well as non-additive effects.

Bhatt (1971) reported combining ability estimates for earliness, plant height and four yield components in a 5 x 5 wheat diallel. The analysis of GCA indicated that the larger portion of the genetic variation, for six out of seven characters considered, was associated with additive gene effects. The estimates of SCA's were highly significant but lower than GCA's for five characters.

Bitzer *et al* (1971) performed a combining ability analysis in a 6 x 6 diallel and found that GCA mean squares were significant for earliness, plant height and kernels per spike whereas SCA mean squares

were not. The average yield of the F_1's was 28.1% higher than that of the highest yielding parent.

Paroda and Joshi (1970a) compared the combining ability variances of F_1 and F_2 generations for yield and other characters in a 6 x 6 wheat diallel. The GCA effects were high in the F_1's and F_2's but SCA effects were high only in F_1's. Similar results were also reported by Niehaus and Pickett (1966) in a *sorghum* diallel.

In some of the papers it has been reported that the parents with high GCA values do not necessarily produce hybrids with high SCA values (Larson, 1941 in tomatoes; Crumpacker and Urquhart, 1962 in wheat; Walker 1963, Chang 1967, Soomro 1967, Baluch and Soomro 1969 and Soomro and Baluch 1969 in cotton). It follows, therefore, that the general combining ability should not be taken as a criterion for predicting high specific combining ability.

Genotype-environment interaction

Finlay and Wilkinson's (1963) regression analysis technique permitted for the first time a satisfactory assessment of the performance stability of a strain or cultivar over the range of environments in which it is grown. According to these authors, a regression of varietal-mean-yield on location-mean-yield with a regression coefficient of less than unity indicates that the variety has an above-average stability in its response to environmental influences. Regression coefficients equal to and greater than unity indicate average and less-than-average stability respectively. Eberhart and Russell (1966) interpreted stability in a

different manner, stating that the Finlay-Wilkinson model implies that a stable variety is one which performs relatively well in a poor environment and relatively poor in a favourable one. They proposed that the criteria for stability should be a regression coefficient of unity and minimum deviation from the unit slope. According to them a variety with high mean yield and fulfilling these two criteria would perform well in all the environments.

Another method of genotype-environment interaction analysis, in terms of biometrical genetics, has been developed by Bucio Alanis (1966) and applied to data for two inbred lines of *Nicotiana rustica* grown over a period of sixteen years at two locations. The analysis has shown that the effects of the genotype-environment interaction are linearly related to a particular environmental effect of the genotype. The model, which is essentially an extension of Mather's model (Mather, 1949), was later extended by Bucio Alanis (1966a) to apply to F_1's with identical and consistent results for this generation also.

For the analysis of genotype-environment interaction by means of the diallel cross, three papers have appeared, one theoretical (Perkins, 1970) and two experimental (Allard, 1956; Crumpacker and Allard, 1962) and are concerned with assessing the stability of genetic components of variation under different environments.

Crumpacker and Allard (1962) studied genotype-environment interaction for heading date in a 10 x 10 wheat diallel over three years. The analysis of variance of heading time for parental genotypes indicated different additive and/or epistatic effects in different years. Because

of the homozygosity of the parents, the epistatic effects attributable to parents were defined by the authors as the result of interaction between homozygous loci, that is, additive x additive type of interaction. Stability of average degree of dominance was tested by the variance ratio for the dominance x year interaction. This was highly significant and showed that the mean degree of dominance for heading date varied from partial to complete dominance in consecutive years.

Porceddu (1968) in a yield test of three wheat varieties over twenty consecutive years at one location showed significant differences between varieties in different years. The results established that the performance of an individual genotype is a linear function of the environment, and that the major portion of the genotype-environment interaction could be accounted for by deviations from the linear response as estimated by the regression analysis.

Baker (1969), analysing the yield of six wheat varieties grown at nine locations over five years, subdivided the sum of squares for genotype-environment interaction into genotype x place, genotype x year and genotype x place x year interactions for each variety. Except for genotype x year, all interactions were highly significant, leading to the conclusion that the stability of performance of a particular cultivar over a range of environments is inversely proportional to the sum of squares for genotype-environment interaction for that particular variety.

Kaltsikes and Larter (1970) analysed genotype-environment interaction for height, maturity and yield in durum wheat. Five varieties

grown over four to five years at five loctions, differed with different environments in all the characters studied. In their analysis, the major portion of the genotype-environment interaction effects was reported to be linearly correlated with the environment.

A considerable amount of work has been reported on genotype-environment interaction analysis with respect to a variety of quantitative characters in different crops (Allard 1961, Parson and Allard 1960, Allard and Workman 1963, in lima-beans; Eagles 1967, Knight 1965, 1970 and Breese 1969, in grasses; Westerman 1970, 1971a, b, in *Arabidopsis*; Hill and Perkins 1969, Perkins and Jinks 1970, 1971a, b, in tobacco; Kaltsikes 1970, in winter rye; Liang and Walter 1966, in *sorghum* and Qualset 1968, and Paroda and Hayes 1957, in barley). In each of these papers, the behaviour of a particular genotype when grown in a particular environment, and when grown with other genotypes over a wide range of environments, is studied using linear regression analysis to measure the environmental effect. The implication of these studies is that the linear regressions of individual genotypic values on the mean values of all genotypes for each of the environments provide measures of the response that are useful in predicting the relative performance of the genotype in question over the range of environmental conditions. The conclusion of these reports focuses on one point: that the performance of an individual genotype in a particular environment is a linear function of the over-all environmental mean in regression analysis, where the slope of regression measures the sensitivity of the genotype to the totality of the environmental factors.

MATERIAL AND METHODS

Five cultivars of common wheat (*Triticum aestivum* L.) described in Appedix I, were used in the diallel study. These varieties were selected on the basis of their diversity of origin, different spike and seed characteristics and their yield performances. The parental material was sown in September 1969 in the green-house to check its trueness to type. Fifteen to twenty phenotypically identical healthy heads were selected from each variety and their seed formed the basis of the present investigations. The parent lines were sown in the green house in January 1970. Crosses were made in all possible combinations, including reciprocals. During summer 1970, the parent material was again seeded at Parkland farm to obtain more F_1 seed. Following the winter, some of the F_1 seeds together with their parents were sown in growth chambers to make backcrosses, reciprocal backcrosses, further F_1 combinations and to provide F_2 seed. During 1971's spring the same procedure was repeated to have sufficient number of seeds for every combination. In the fall of 1971, the backcrosses and their reciprocals were seeded in the growth chambers to obtain seed for their first selfed generation.

By spring 1972, the experimental material consisted of five parents, 20 F_1's, 20 F_2's, 80 backcrosses and the selfed generation of these backcrosses, amounting to 205 different entries. A 15 x 15 partially balanced lattice design was chosen for seeding the material in a replicated trial. To meet the requirements of the design, 20 more entries were needed and since the F_2 is the maximum segregation generation,

each F_2 combination was represented twice in each replication to complete the required 225 entries. The names and numerical designations of the entries are given in Appendix II. On 9th and 11th May, 1972, the whole of the experimental material was space-seeded in three replications at two locations, viz., Department of Genetics Ellerslie Field Lab. and Department of Plant Science Parkland Farm, respectively. Each of the fifteen (15' x 15') blocks in a replication consisted of 15 rows of 30 seeds each, with a spacing of 30.48 cm between rows and 15.24 cm between seeds within a row. The following observations were recorded at each of the locations:

(1) Onset-of-heading: expressed as the number of days between seeding date and the date of appearance of the first head in the row (entry).

(2) Final heading: recorded in number of days from the date of seeding to the day when 75% of the plants in a row have headed.

(3) Heading-span: measured by the difference between (1) and (2).

(4) Plant height: measured in centimeters from the surface of the soil to the tip of the spike on the highest tiller (excluding awns). Ten consecutive plants per row were recorded for height irrespective of their growth performance, leaving the first plant because of susceptibility to border effects, except in those rows where the number of surviving plants was reduced to ten or less. At maturity only those

plants that had been recorded for height were harvested. The following observations for yield and yield components were recorded on the harvested material.

(5) Number of productive tillers per plant.

(6) Number of spikelets per spike: Three spikes were taken at random from each plant and their spikelets counted.

(7) Number of seeds per spike.

(8) Weight of seeds per spike (in grams): spikes randomly sampled for spikelet-counts were threshed separately and their seeds counted and weighed.

(9) 1000-kernel weight (in grams): computed from observations (7) and (8).

(10) Yield per plant (in grams): expressed as total seed weight of all the spikes including those used for (6), (7), and (8).

Statistical analysis

The means were calculated for all the characters except onset-of-heading, final heading and heading-span. For observations (6), (7) and (8) means of three readings were calculated first and treated as individual variables for the calculation of entry means. Missing entries were calculated according to Cochran and Cox's (1957) formula for the randomized block design, except for (1) to (4) at Parkland. Here, since the number of missing entries was less than three, the procedure for the partially balanced lattice design was used. The complete set of data was subjected to analysis of variance for a partially balanced lattice design. This provided a single set of adjusted treatment means at each location. However, unadjusted treatment means (original entry

means as treated in randomized block design) were used for most of the analyses. These were categorized into four diallel sets, viz., F_1's, F_2's, backcrosses and selfed backcrosses. The following analyses were performed on each of the sets for all the characters under study.

1. Correlation and factor analyses. Simple correlation coefficients were computed for each of the characters and arranged in the form of a matrix to permit the simultaneous comparison of one character with the other. Factor analysis was performed according to Hotelling's (1933) principal factor method as explained by Harman (1960) and Lawley and Maxwell (1963). The factor analysis approach aims at resolving the covariation into simpler relations in the form of a few factors which explain the larger portion of the variation in the original data. Statistically speaking, it reduces a large number of correlated variables to a small number of uncorrelated variables called factors, each of which proportionally accounts for the variability in the original observations.

The procedure for the principal factor method used in the present study was based on the following linear model (Harman, 1960):

$$z_j = a_{j1}F_1 + a_{j2}F_2 + \ldots\ldots + a_{jm}F_m + d_j u_j. \quad (j = 1, 2, \ldots, n)$$

where z_j represents a character variable in terms of several underlying factors and each of the 'n' observed variables is described linearly in terms of 'm' common factors and the residual error ($d_j u_j$). The coefficients of these factors are referred to as factor loadings. A symmetrical correlation matrix produced from all possible [1/2n(n - 1)] combinations is resolved into an 'nk' factor matrix, where the number of factors 'k' is usually smaller than 'n', the number of variables.

In the correlation matrix, the leading diagonal elements have values of unity and since they are meaningless (the correlation of each variable with itself means nothing) they are replaced by 'communalities' (the approximate values in terms of amount of variance accounted for by the common factors). In the present case the highest correlation value in each column of the correlation matrix was substituted for unity in the diagonal cells because the variance-covariance ratio of the column for that character is expected to be nearer to unity. With these communalities as the approximate values, the correlation matrix was factored by iteration to give a new resultant set of approximations to communalities that are more convergent. The factor matrix was then rotated (in this case by the varimax method) with every new set of communalities produced, till off-the-diagonal elements of the residual matrix were not significantly different from zero.

2. Combining ability analysis. General and specific combining ability analyses were performed following Griffing's (1956) method 1 (where all the n^2 entries of the diallel table are included), model 1 (where the experimental material is not regarded as a random sample from the population). Model 1 was chosen against model 2 (where the experimental material is regarded as a random sample from the population) because the parental lines, producing all the entries in the form of various combinations, were deliberately chosen on the basis of their diversity of origin and yielding capacities.

3. Diallel cross analysis. Diallel analysis was performed in two steps,

viz., diallel analysis for genetic components of variation and graphical analysis of regression of W_r (parent-offspring covariance of the rth. array) on V_r (variance of the rth. array) to complement the former via graphical representation. In the diallel analysis for genetic components of variation, each diallel table was subjected to tests of validity of the following assumptions (Hayman, 1954b):

(1) Homozygous parents

(2) Normal diploid segregation

(3) No differences between the reciprocal crosses

(4) No multiple allelism

(5) Independent action of non-allelic genes

(6) Uncorrelated gene distribution.

The condition of 'homozygous parents' in the present studies could be satisfied, as the parent material was sown preceding crossing and found to be true to type. 'Normal diploid segregation' may be assured from the pedigree-record of the organism used as experimental material. Wheat, though an amphi-diploid derivative of *Triticum monococcum* for the 'A' genome (Melburne and Thompson, 1927; Zohary and Feldman, 1962), *Aegilops speltoides* for the 'B' genome (Sarkar and Stebbins, 1956; Riley *et al*, 1958; Sears and Okamoto, 1958) and *Aegilops squarrosa* for the 'D' genome (Kihara, 1944; McFadden and Sears, 1944, 1946; Kihara and Lilienfeld, 1949) behaves cytogenetically as a normal diploid (Sears, 1948; Riley *et al*, 1961). It follows therefore, that, the assumption of normal diploid segregation could be considered valid. 'No reciprocal differences' were checked after Hayman's (1954a) procedure

of analysis of variance for diallel tables, where significance of the 'c' component indicates failure of this hypothesis. The remaining three conditions, 'no multiple allelism', 'independent action of non-allelic genes' and 'uncorrelated gene distribution' were checked through the analysis of variance of $W_r - V_r$ values for the arrays of each diallel table. Heterogeneity of $W_r - V_r$ variances will reveal non-validity of these assumptions.

After the validity checks for the above-mentioned conditions, the diallel analysis for genetic components of variation (Hayman 1954b, 1958 and Jinks 1954, 1956) was performed, on each of the diallel tables for all the characters under study, by replacing the off-diagonal cells of the diallel table with the common mean of the relevant cross and its reciprocal irrespective of the significance of Hayman's (1954a) 'c' component. In the F_2-generation diallel, the estimates of genetic components of variation from the second degree statistics were computed after Johnson and Aksel's (1959) notation describing the average effect of Aa in different filial generations. According to their formula:

$$\text{effect of } Aa = [(1/2)^{fn-1} h]$$

where fn = nth filial generation

$$\text{thus in } F_2, \text{ effect of } Aa = [(1/2)^{2-1} h]$$

$$\text{and in } F_3, \text{ the effect of } Aa = [(1/2)^{3-1} h] \text{ and so on.}$$

From the genetic components of variation, various parameters such as the mean degree of dominance, the proportion of positive to negative alleles at loci exhibiting dominance, the ratio of dominant to recessive genes in the parents

and the number of groups of genes controlling the particular character were estimated. The heritability estimates were calculated after Crumpacker and Allard (1962) using the formula $[D \div (D + H_1 - F + 4E)]$.

The graphical analysis of regression of W_r on V_r was performed after Hayman (1954b) by plotting the regression line and the limiting parabola constructed by calculating its points $(W_r 2 = V_r \times V_{OLO})$ and plotting the V_r, $(W_r \times V_{OLO})^{1/2}$ points. The W_r, V_r graphs were supplemented with Johnson and Aksel's (1959) standardized deviation graphs of parental measurements (Y_r) and parental order of dominance $(W_r + V_r)$ where the deviations of the Y_r's and $W_r + V_r$'s from their respective means were standardized by dividing them by their respective standard deviations. An abscissa (Y_r) and an ordinate $(W_r + V_r)$ intersecting each other produce four quadrants of the graph, classified as (+,+), (−,+), (−,−) and (+,−). The plus and minus signs for $(W_r + V_r)$ denote 'recessive' and 'dominant' and for Y_r, they refer to 'high' and 'low' performances respectively.

4. Analysis of genotype-environment interaction. The constancy of principal factors with respect to loadings in four generations of diallel cross was studied by means of *factorial ANOVA* where locations, principal factors and generations were treated as main source of variation. The *ANOVA* was based on fixed-effect-model as described by Scheffe (1959) because the set of parents in all the diallel tables could not be regarded as random sample and the two locations at which the materials were grown could not be considered as representing

random sample of the environments. Their choice was dictated by the limitations imposed both by time and facilities available.

The differences between the two locations with respect to general combining ability were also studied by *factorial ANOVA*. Stability of each cultivar was determined by regressing its GCA at Parkland upon that at Ellerslie. The regression analysis used was as given by Mather (1951).

The genotype-environment interaction with respect to D, H_1 and F considered as variables was investigated by using factorial analysis of variance. The concordance of the components in the two locations was studied by regressing the values of D, H_1 and F estimated from Parkland data upon those of Ellerslie and partitioning the total sum of squares into sum of squares due to regression and due to deviation from regression (error). Diallel analysis for genetic components of variation from adjusted treatment means (balanced lattice design) was compared with that of unadjusted treatment means (experiment treated as a randomized block design). The differences between the parameter estimates would reflect the effect of the adjustment factor characteristic of partially balanced lattice design. The regression analysis (Mather, 1951) applied to D, H_1 and F obtained from both the adjusted and unadjusted treatment means, will reveal the degree of concordance between the parameters characteristic of each treatment.

EXPERIMENTAL RESULTS

The experimental data for the two locations; (1) Ellerslie and (2) Parkland, are given in Appendices III to XXII inclusive. Table 1 shows the results of the analysis of variance of the partially balanced lattice design and its efficiency as compared to the analysis as a randomized block. The mean squares of the adjusted treatments except for number of tillers per plant and yield per plant, both at Parkland, all showed significant differences among the entries. The relative efficiency of the balanced lattice design at Parkland over the randomized block design was greater than that at Ellerslie.

ANALYSIS OF F_1 DATA

Simple correlations were computed for all the characters under study and are given in Table 2. As shown in the table:

Onset-of-heading was positively correlated with plant height and number of spikelets per spike and negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. At Ellerslie, it was positively correlated with final heading and negatively with yield per plant, while at Parkland, it showed positive correlation with number of tillers per plant and number of seeds per spike. The negative correlation of onset-of-heading with yield, weight of seeds per spike and 1000-kernel weight indicates that the longer the period between seeding and the appearance of the first head for a particular entry, the lower will be its yield and 1000-kernel weight. Correlations of final heading and heading-span with other characters may be interpreted in the same fashion.

TABLE 1

Mean-square values from the analysis of variance of partially balanced triple lattice design with respect to ten characters at two locations

Character	Replication	Blocks within replications	Treatments (adjusted)	Error	Total sum of squares	% Efficiency over randomized block
†D.F.	2	42	224	406	674	
Onset-of-heading	5.7305	4.9140**	10.3581**	1.0209	2948.5180	119.205
	19.8980	18.1369**	18.2897**	2.5313	5921.1450	127.013
Final heading	14.4640	8.0242**	17.3218**	1.4999	4849.0160	118.699
	204.9375	14.7080**	19.2502**	3.1787	6601.6170	108.332
Heading-span	24.0635	2.8539*	3.1996*	1.6111	1532.3940	95.829
	137.0770	6.6719**	4.6495**	2.6398	2662.3760	107.162
Plant height	273.8125	566.9384**	543.1358**	41.0030	162503.6250	121.334
	1017.5480	524.6927**	738.0608**	129.1721	241583.5620	99.301
Number of tillers per plant	0.9950	4.8374	4.6147	5.6567	3495.9080	87.318
	133.0380	10.5493**	6.0799**	3.0278	3288.2760	109.575
Number of spikelets per spike	10.8070	2.5932**	1.8178*	1.3783	1087.8420	85.553
	19.9485	4.1922**	2.2189**	1.0273	1125.9980	109.766
Number of seeds per spike	10.0065	50.2140**	39.1424**	18.5529	18299.5550	91.021
	180.0355	36.4799**	25.7529**	11.9034	12446.094	100.465
Weight of seeds per spike	0.0060	0.0095**	0.0843*	0.0455	41.2460	90.426
	0.0940	0.0942**	0.0586*	0.0321	30.2060	104.704
1000-kernel weight	12.2045	21.8132**	18.7903**	8.4791	8616.7660	90.954
	35.3210	25.9427**	17.5137**	7.8801	8251.1520	104.127
Yield per plant	16.1310	20.8652*	10.3075	15.8876	9556.6840	86.462
	153.8140	18.2453**	8.3171*	6.2202	5431.8160	104.334

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level
** Significant at 1% level
† Corresponding to the missing values in the different characters, the number of degrees of freedom have been subtracted from error D.F. in calculating mean squares.

Plant height was positively correlated with number of spikelets per spike and negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. It was positively correlated with number of tillers per plant at Ellerslie while at Parkland the correlation coefficient was not significant.

Number of tillers per plant was positively correlated with yield per plant at both locations and with number of spikelets per spike at Ellerslie. Correlation of number of tillers per plant with number of seeds per spike, weight of seeds per spike and 1000-kernel weight was not significant at either location. The correlation coefficients of other components of yield, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight could be explained in the same manner.

As far as yield is concerned, it was highly and positively correlated with 1000-kernel weight, weight of seeds per spike and number of tillers per plant at both locations, but negatively correlated with onset-of-heading and final heading at Ellerslie.

Factor analysis

In the factor analysis, the symmetrical correlation matrix produced for all the characters under study was resolved into a varimax-rotated factor matrix. As suggested by Cattel (1965), if the number of factors is kept equal to that of the variables, 100% of the covariation in the data could be accounted for by these factors. In the present case the data was computerized for five factors which explained 92% of the

TABLE 2

Simple correlation coefficients between ten characters from F_1 diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.916**	0.196	0.723**	0.145	0.313**	0.191	-0.324**	-0.615**	-0.281**
	0.082	0.028	0.821**	0.291**	0.545**	0.246**	-0.304**	-0.612**	-0.150
2. Final heading	-	0.548**	0.744**	0.196	0.257**	0.150	-0.331**	-0.574**	-0.278**
		0.618**	0.790**	0.358**	0.588**	0.267*	-0.240*	-0.547**	-0.058
3. Heading-span		-	0.316**	0.166	-0.022	-0.012	-0.135	-0.146	-0.147
			0.241*	0.219	0.270*	0.122	-0.006	-0.114	0.105
4. Plant height			-	0.365**	0.416**	0.149	-0.250*	-0.474**	-0.026
				0.239	0.601**	0.106	-0.402**	-0.612**	-0.162
5. Number of tillers per plant				-	0.272*	-0.014	0.059	0.117	0.574**
					0.194	0.085	-0.039	-0.121	0.320**
6. Number of spikelets per spike					-	0.582**	0.280*	-0.225	0.154
						0.556**	0.206	-0.207	0.184
7. Number of seeds per spike						-	0.663**	-0.165	0.144
							0.659**	-0.014	0.211
8. Weight of seeds per spike							-	0.624**	0.502**
								0.740**	0.506**
9. 1000-kernel weight								-	0.512**
									0.500**
10. Yield per plant									-

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level
**Significant at 1% level

total variability with respect to all the characters at respective locations. The values of the rotated factor matrix in terms of the factor loadings together with the communalities for ten characters are given in Table 3.

The first factor was termed *lateness* because it carried the highest loadings for onset-of-heading and final heading at both locations and explained 28% and 32% of the variation in the data at Ellerslie and Parkland. Yield per plant was negatively affected by this factor showing thus that higher the number of days taken by a particular entry to head the larger will be its contribution to *lateness* and lower will be its yield and 1000-kernel weight. Plant height was one of the major contributors to *lateness* as it carried high loadings at both locations. This corresponds proportionally to the positive association between days to head and height of the plant. Number of tillers per plant, number of spikelets per spike and number of seeds per spike contributed very little to this factor.

The second principal factor was termed *yielding ability* as it carried generally higher loadings for yield and yield components: spikelets per spike, number of seeds per spike and, (except at Ellerslie) 1000-kernel weight at both locations. This factor accounted for about 19% of the variation. The loadings on yield and its components for this factor, as against those of the first factor (*lateness*), support a negative relationship between lateness and yielding ability. There is very little contribution of plant height and number of tillers per plant for this factor at either location.

TABLE 3

Varimax rotated factor matrix for ten characters from F_1 diallel set at two locations

Character	Communalities	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.964	0.960	0.107	-0.060	-0.167	-0.010
	0.908	0.892	-0.242	0.062	-0.093	0.205
Final heading	0.972	0.901	0.070	-0.022	-0.153	0.363
	0.945	0.773	-0.173	0.073	0.516	0.212
Heading-span	0.994	0.215	-0.040	0.033	-0.032	0.972
	1.000	0.123	0.032	0.039	0.987	0.086
Plant height	0.806	0.788	0.175	0.294	-0.224	0.139
	0.906	0.917	-0.174	-0.113	0.132	0.066
Number of tillers per plant	0.886	0.182	0.038	0.915	-0.010	0.121
	0.961	0.177	0.126	0.807	0.113	0.949
Number of spikelets per spike	0.867	0.188	0.847	0.282	-0.182	-0.047
	0.824	0.756	0.199	0.431	0.160	-0.039
Number of seeds per spike	0.923	0.160	0.882	-0.133	0.321	0.005
	0.971	0.218	0.626	0.957	0.050	0.061
Weight of seeds per spike	0.990	-0.249	0.523	0.086	0.804	-0.034
	0.963	-0.258	0.567	0.754	-0.012	-0.088
1000-kernel weight	0.884	-0.486	-0.227	0.268	0.724	-0.030
	0.878	-0.518	0.747	0.143	-0.060	-0.169
Yield per plant	0.851	-0.170	0.109	0.762	0.456	-0.145
	0.863	0.011	0.876	0.114	0.043	0.282
Percent of total variability explained	91.396	28.203	18.808	16.589	16.165	11.361
	92.187	32.355	18.226	17.273	13.131	11.202

First reading under each column refers to Ellerslie and the second to Parkland.

The term *tillering-capacity* was chosen for the third principal factor, as the number of tillers per plant contributed highest at both locations. The factor explains approximately 17% of the total variation and is supported by number of spikelets per spike, number of seeds per spike (at Parkland), weight of seeds per spike, 1000-kernel weight and yield per plant. Since this component is closely associated with the *yielding-ability*, the *lateness* factor shows negative effects for onset-of-heading and final heading. This kind of response seems to be logical since high tillering capacity results in higher yield per plant and is associated with earliness.

The fourth principal component, named *heading-period* at Parkland and *seed weight* at Ellerslie, accounted for 13% and 16% of the variation respectively. Different names were chosen for different locations because of the inconsistency between locations of factor loadings on various characters. At Ellerslie, the *seed-weight* component was affected by number of seeds per spike, 1000-kernel weight and yield per plant. The contribution of onset-of-heading, final heading, heading-span, plant height and number of tillers per plant towards this component was negative. At Parkland, *heading-period* was positively affected by final heading, plant height, number of tillers per plant and number of spikelets per spike.

The terms *heading-period* and *tillering-capacity* were also used for fifth principal component at Ellerslie and Parkland, respectively, because of their high contribution towards the loadings of this factor. Only 11% of the total variability was accounted for by this factor at both

TABLE 4

Estimates of general combining ability
of five parental lines used in F_1 diallel set
for ten characters at two locations

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.933	1.4667	-0.4666	-1.7334	-1.2000
	1.9867	2.3533	-0.8800	-2.2466	-1.2133
Final heading	2.1600	1.7934	-0.3733	-2.1066	-1.4733
	2.4800	2.9466	-1.0867	-2.4867	-1.8533
Heading-span	0.2600	0.3933	0.1267	-0.4400	-0.3400
	0.4800	0.5800	-0.2200	-0.2200	-0.6200
Plant height	13.7470	12.1740	-8.1473	-7.8220	-9.9516
	12.3968	13.4648	-8.7599	-7.9252	-9.1766
Number of tiller per plant	-0.0409	0.8629	0.6390	-0.3116	-1.1495
	0.3351	0.3316	0.5466	-0.1349	-1.0784
Number of spikelets per spike	0.5123	0.3536	-0.5752	-0.3151	0.0245
	0.6729	0.4595	-0.5058	-0.3616	-0.2650
Number of seeds per spike	2.8305	-1.5451	-1.1460	-1.9094	1.7700
	2.0515	-0.9495	0.3450	-2.4385	0.9916
Weight of seeds per spike	-0.0103	-0.1285	-0.0092	0.0008	0.1472
	-0.0326	-0.0958	0.0848	-0.0501	0.0938
1000-kernel weight	-2.4230	-1.5338	0.7291	1.7007	1.5269
	-2.3256	-1.3217	1.6523	0.8898	1.1052
Yield per plant	-0.1646	-1.2333	-0.0382	0.1903	1.2458
	-0.4672	-0.5154	0.3461	0.2629	0.3736

First reading under each column refers to Ellerslie and the second to Parkland.

locations. The factor was negatively affected by number of spikelets per spike, weight of seeds per spike and 1000-kernel weight.

Combining ability analysis

Estimates of general and specific combining ability for the F_1 diallel were obtained by Griffing's (1956) procedure following method 1, model 1. General combining ability (GCA) values for all the characters at both locations are given in Table 4. Marquis appeared to be the best combiner for onset-of-heading, final heading, plant height, number of spikelets per spike and number of seeds per spike at both locations. For tillering capacity Chinook exhibited the highest combining ability at Ellerslie while Khush-hal excelled Chinook at Parkland. Inia showed the highest general combining ability for yield per plant, 1000-kernel weight and weight of seeds per spike at both locations. It is interesting to note that Inia excelled Marquis and Chinook (both Canadian standard varieties) in general combining ability for yield in a foreign environment. This might be attributed to a better adaptability of Inia as compared to the other two introductions, viz., Khush-hal and Ciano, of Pakistan and Mexican origin. Generally it could be said that Canadian environments are less suitable for introductions like Khush-hal and Ciano as far as yield per plant is concerned.

The values of specific combining ability (SCA), reciprocal effects and variances for general and specific combining abilities for F_1 hybrids are given in Tables 5 to 15.

Cross (CxI) had the highest SCA for onset-of-heading (Table 5),

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_1 diallel set at two locations.

TABLE 5. Onset-of-heading

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.8667 0.6801	-0.5333 -0.0866	-1.1000 -0.8866	-1.2999 -1.2533	1.9333 1.9867	3.6535 3.7430	-0.2104 -0.5095
Chinook	Reciprocal effects	-0.3333 0.1667	-	-0.9000 0.3800	-0.4667 0.2467	-0.5000 -1.1200	1.4667 2.3533	2.0669 5.3343	0.0400 -0.3554
Khush-hal		0.0 -0.1667	-0.5000 0.0	-	0.1333 -0.6867	0.4333 -0.8867	-0.4666 -0.8800	0.1336 0.5705	0.1544 -0.4589
Ciano		-0.5000 -2.0000**	0.0 -0.1667	0.6667 0.0	-	1.0334 0.9800	-1.7334 -2.2466	2.9204 4.8435	0.2715 -0.0701
Inia		0.5000 1.0000	0.5000 0.1667	0.8333* -0.5000	-0.1667 1.0000	-	-1.2000 -1.2133	1.3558 1.2683	0.8548 1.0144

TABLE 6. Final heading

Marquis		-	1.0733 2.9200	-0.9267 -1.7133	-1.3600 -1.4799	-1.6000 -1.4467	2.1600 2.4800	4.5722 5.8974	-0.2335 -0.6322
Chinook		0.0 0.0	-	-0.8934 -1.6799	-0.3267 -1.2800	-0.2933 -2.0800	1.7934 2.9466	3.1227 8.4298	0.1505 2.2100
Khush-hal	Reciprocal effects	-0.5000 0.3333	-0.5000 -0.1667	-	-0.4933 0.2534	-0.1266 0.6200	-0.3733 -1.0867	0.0459 0.9280	0.3187 1.2870
Ciano		-0.3333 -1.1667	0.0 -1.1667	0.0 0.0	-	0.9400 1.1867	-2.1066 -2.4867	4.3445 5.9306	0.4979 0.6653
Inia		0.8333 0.1667	0.0 0.0	0.0 0.0	0.0 -0.1667	-	-1.4733 -1.8533	2.0773 3.1819	0.5436 2.1050

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

at both locations followed by hybrid (MxCH). This shows that hybrid (CxI) was latest in heading and implicitly in maturity. Cross (MxI) exhibited lowest SCA and hence could be regarded as the earliest of all the F_1's. It is interesting to note that for both locations, the best hybrid, with the highest SCA, had parents showing the lowest GCA's, while the poorest hybrid, with the lowest SCA, had the female parent with the highest GCA and the male parent with the lowest GCA. Thus it appears unlikely that the best performing parents (those with high GCA's) necessarily produce hybrids showing high SCA's. None of the hybrids showed significant reciprocal effects except (IxK) at Ellerslie and (CxM) at Parkland, and the parental variances for GCA were in general higher than for SCA.

With respect to final heading (Table 6) and heading-span (Table 7), although there are some differences in relative positions of the parents and hybrids concerned, the general conclusions are the same as for onset-of-heading.

With respect to highest SCA for plant height (Table 8) at both locations, the best hybrid was (MxCH) and the poorest (MxI). The parents of cross (MxCH) had the highest GCA at both locations while the poorest hybrid had Marquis as one parent, with the highest GCA and Inia as the other, with the lowest GCA. The parental GCA-variances were larger than their SCA-variances at both locations, suggesting a greater importance of additive gene effects for the parental lines than of non-additive ones for the hybrids, with respect to plant height. The reciprocal effects were significant for (CxM) at both locations and for (IxM) and (IxCH) at Ellerslie. In the case of (IxM), the reciprocal effects could be attributed

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_1 diallel set at two locations.

TABLE 7. Heading-span

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	2.2533 0.0400	-1.6133 -0.0267	-0.6133 -0.2933	-0.2133 0.1067	0.4800 0.2600	-0.0163 -0.1184	-0.2096 -0.8721
Chinook		-0.1667 0.3333	-	-2.0467 -0.1600	-1.5467 0.0733	-0.9800 0.1400	0.5800 0.3933	0.0709 -0.0124	-0.2091 0.8204
Khush-hal		0.5000 0.0	-0.1667 0.0	-	0.9200 -0.6600	1.4867 -0.5933	-0.2200 0.1267	-0.0678 -0.3004	-0.2009 1.3018
Ciano		0.8333* 0.1667	0.0 0.0	0.0 -0.6667	-	0.3200 -0.0267	-0.2200 -0.4400	0.1097 -0.3004	-0.0340 -0.3328
Inia		-0.8333* 0.3333	-0.1667 -0.5000	0.5000 -0.8333	-1.3333** 0.1667	-	-0.6200 -0.3400	0.0317 0.0356	-0.0817 0.2341

Reciprocal effects

TABLE 8. Plant height

Marquis		-	3.4117 3.6766	2.0390 2.7912	-2.3879 -1.9234	-4.1067 -4.4220	13.7470 12.3968	187.1822 151.7148	-4.4931 -4.9129
Chinook		0.2933 -0.1134	-	2.4237 1.5132	1.3784 3.0219	2.6996 -3.3567	12.1740 13.4648	146.4086 179.3356	-0.5994 -0.4071
Khush-hal		-0.4766 1.2467	0.8250 1.8566	-	-1.9553 -0.1367	-0.0704 -0.0287	-8.1473 -8.7599	64.5814 74.7702	-1.1491 -1.5526
Ciano		-3.7717* -4.3133	-1.3083 -0.7933	0.9233 1.3100	-	1.3890 2.0900	-7.8220 -7.9252	59.3868 60.8436	-0.6846 -0.6295
Inia		5.1567** 3.3467	-4.5567* -1.4767	1.0980 2.1400	-2.0700 -0.5600	-	-9.9516 -9.1766	97.2374 82.2441	4.4238 6.8172

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.
* Significant at 5% level
**Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_1 diallel set at two locations.

TABLE 9. Number of tillers per plant

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	-0.0903	-0.7628	0.5342	-0.1946	-0.0409	-0.3273	-0.8224
			-0.8068	-1.2051	-0.3143	-1.1968	0.3351	-0.1992	-0.7787
Chinook		1.1667	-	1.8354	-0.1528	-0.4983	0.8629	0.4155	-0.8197
		0.0667		0.5318	-0.5535	-0.3683	0.3316	-0.2015	-0.5617
Khush-hal		-0.4297	0.1055	-	-0.3790	-0.3183	0.6390	0.0794	0.4944
		1.0167	-0.6833		0.5982	-0.0249	0.5466	-0.0127	-0.2004
Ciano		0.4833	-0.5000	0.7833	-	0.5094	-0.3116	-0.2319	-0.6716
		0.1593	-1.1167	0.6167		1.0399	-0.1349	-0.2933	-0.5244
Inia		-0.4500	-1.2500	0.8227	0.3500	-	-1.1495	0.9923	-0.6077
		0.6000	0.4083	0.4167	-0.7333		-1.0784	0.8513	0.1064

Reciprocal effects

TABLE 10. Number of spikelets per spike

Marquis		-	-0.2740	0.1741	-0.0388	-0.4728	0.5123	0.1150	-0.3687
			1.1008	-0.2395	-0.1238	-0.1136	0.6729	0.3652	-0.2192
Chinook		-0.3333	-	0.2618	0.3642	-0.0032	0.3536	-0.0224	-0.3436
		0.2668		0.1404	-0.1925	-0.5073	0.4595	0.1235	0.1847
Khush-hal		1.0593	-0.2623	-	-0.3403	-0.1155	-0.5752	0.1834	-0.3357
		-0.3278	-0.3167		0.1615	-0.3017	-0.5058	0.1682	-0.1935
Ciano		-0.0778	-0.1002	0.4888	-	0.2157	-0.3151	-0.0482	-0.2854
		-0.4012	-0.0277	0.2057		0.5208	-0.3616	0.0431	-0.1931
Inia		-0.4388	0.1947	0.4692	0.0222	-	0.0245	-0.1469	-0.2742
		-0.2390	0.3458	0.1447	-0.2168		-0.2650	-0.0175	-0.0073

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_1 diallel set at two locations.

TABLE 11. Number of seeds per spike

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	-1.9659 1.2486	2.2792 0.1486	0.9872 -1.2352	-3.1363 1.7185	2.8305 2.0515	6.6103 3.1165	-3.5029 -2.7300
Chinook	Reciprocal effects	-0.6665 0.1168	-	0.0151 0.1107	0.9075 -0.3172	2.0447 0.1696	-1.5451 -0.9495	0.9862 -0.1904	-2.2146 -2.2104
Khush-hal		3.1140 1.5667	-1.3513 -0.7168	-	-2.5752 -0.1725	-0.3525 -2.4527	-1.1460 0.3450	-0.0878 -0.9730	-1.7712 -2.2186
Ciano		4.5557** 0.4772	1.7223 0.5945	-0.6055 1.0333	-	2.9756 1.9031	-1.9094 -2.4385	2.2445 4.8542	-0.6930 -2.1780
Inia		-1.5222 -1.1278	0.0723 1.5223	-0.7965 -0.8835	-2.2833 -1.1335	-	1.7700 0.9916	1.7317 -0.1088	4.1624 1.4764

TABLE 12. Weight of seeds per spike

Marquis		-	-0.0905 0.0512	0.0739 -0.0038	0.1517 0.0746	-0.1100 0.0983	-0.0103 -0.0326	-0.0032 -0.0027	-0.0083 -0.0095
Chinook	Reciprocal effects	-0.0175 -0.0320	-	0.0364 0.0194	0.0412 -0.0762	0.0439 0.0399	-0.1285 -0.0958	0.0132 0.0054	-0.0056 -0.0087
Khush-hal		0.1782* -0.0287	-0.0768 -0.0527	-	-0.1029 0.0249	0.0727 -0.0356	-0.0092 0.0846	-0.0033 0.0034	-0.0061 -0.0094
Ciano		0.2843** 0.0622	0.0267 0.0268	-0.0705 0.1142	-	0.0391 0.0487	0.0008 -0.0501	-0.0033 -0.0013	0.0036 -0.0055
Inia		-0.0590 -0.0805	-0.1433 -0.0038	0.0425 0.0427	-0.0505 -0.0460	-	0.1472 0.0938	0.0183 0.0050	-0.0014 -0.0046

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_1 diallel set at two locations.

TABLE 13. 1000-kernel weight

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	-0.1201 0.0835	-0.5650 -0.2523	2.0236 2.6151	0.1734 0.8063	-2.4230 -2.3256	-1.0311 -0.2340	-2.6455 -1.2556
Chinook	Reciprocal effects	0.2312 -0.7130	-	0.7965 0.3194	0.0375 -1.5360	-0.7600 0.9759	-1.5338 -1.3217	0.4628 -0.2366	-2.5316 -1.2425
Khush-hal		1.1725 -1.7405	-0.6182 -0.4882	-	0.0280 0.7257	1.8405 1.4420	0.7291 1.6523	-1.0567 -0.3825	-1.1211 -1.2450
Ciano		2.1175 1.0338	-0.9577 0.1613	-1.2283 1.7450	-	-1.5895 -0.4875	1.7007 0.8898	-1.0220 -0.4331	-0.6646 -0.9974
Inia		-0.0403 -1.0033	-3.1908* -1.3335	1.4478 1.8997	0.8910 0.0420	-	1.5269 1.1052	0.4939 -0.3636	-1.2788 -0.9555

TABLE 14. Yield per plant

Marquis		-	-0.5845 -0.1980	-0.9024 0.1755	2.4220 0.8520	-0.3343 0.0911	-0.1646 -0.4672	-1.0311 -0.2840	-2.6455 -1.2556
Chinook	Reciprocal effects	1.1575 -0.6980	-	1.9387 0.0337	0.0545 -0.2106	-0.7460 -0.6938	-1.2330 -0.5154	0.4628 -0.2366	-2.5316 -1.2425
Khush-hal		0.3260 -0.1923	-0.7188 -0.5447	-	-0.2716 -0.0804	1.6500 0.2976	-0.0382 0.3461	-1.0567 -0.3825	-1.1211 -1.2450
Ciano		2.5833 -2.0633*	-0.5388 -0.3382	0.8368 1.6012	-	-0.9329 0.5674	0.1903 0.2629	-1.0220 -0.4331	-0.6646 -0.9974
Inia		-0.2452 -1.0785	-3.2108* -0.0700	0.5890 2.5692*	0.5675 -0.4895	-	1.2458 0.3736	0.4939 -0.3626	-1.2788 -0.9555

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

to the female parent (Inia) while for (CxM) and (IxCH), the male parents Marquis and Chinook are responsible, because of the negative sign associated with the effects.

For number of tillers per plant (Table 9), the hybrids (CHxK) and (CxI) had the highest SCA's at Ellerslie and Parkland respectively. The parental GCA for (CHxK) at Ellerslie was highest whereas that for (CxI) at Parkland was the lowest. The poorest hybrid was (MxK) at both locations, having the lowest SCA value, although one of its parents (Khush-hal) showed high GCA. The variances for GCA were generally higher than those for SCA.

Hybrid (CHxC) at Ellerslie and (MxCH) at Parkland, respectively ranked highest for number of spikelets per spike with respect to their SCA's, whereas cross (MxI) at Ellerslie and (CxI) at Parkland ranked lowest. It could be argued that the hybrid (MxI) had one parent (Marquis) ranking highest in GCA and hybrid (CHxC) had one parent (Ciano) with a very low GCA which shows that high parental GCA's might not result in higher SCA's for the hybrids. In general, the variances for GCA, were higher than those for SCA. The reciprocal effects were non-significant for all crosses.

The interpretation of the results for general and specific combining ability and the reciprocal effects for number of seeds per spike (Table 11), weight of seeds per spike (Table 12), 1000-kernel weight (Table 13) and yield per plant (Table 14) follow the same pattern. Differences may be found with respect to relative positions of the parents and hybrids concerned but the general conclusions are the same.

TABLE 15

Analysis of variance of general and specific combining ability for ten characters from F_1 diallel set at two locations.

Character	M.S. for GCA	M.S. for SCA	M.S. for reciprocal effects	Error M.S.
D.F.	4	10	10	48
Onset-of-heading	26.3438**	1.9125**	0.4556	0.3155
	41.9375**	2.2312**	1.2722	0.7640
Final heading	36.5000**	2.8562**	0.2611	0.3504
	64.0469**	7.1312**	0.3167	0.9482
Heading-span	1.3688**	0.4951	0.3333	0.3144
	2.6199	4.5816**	0.7500	1.3089
Plant height	1409.4062**	22.8000**	14.1257*	6.7393
	1396.7344**	22.6250**	8.6772	7.3723
Number of tillers per plant	6.4326**	1.2214	1.0437	1.2336
	4.2588*	2.6332*	0.8791	1.1674
Number of spikelets per spike	2.0459*	0.2086	0.4016	0.5531
	2.8027**	0.5035	0.1455	0.3284
Number of seeds per spike	46.2188**	9.3219	8.8449	5.2554
	30.4062**	4.4004	2.0571	4.0978
Weight of seeds per spike	0.0959**	0.0169	0.0306*	0.0124
	0.0719**	0.0137	0.0065	0.0142
1000-kernel weight	34.9531**	3.0262	4.3586	3.2919
	29.7500**	5.2500	2.8623	2.7816
Yield per plant	7.8486	3.8074	4.1329	3.9663
	2.0332	0.6977	3.1529	1.8834

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

A general review of the results of the combining ability analyses with respect to all the characters under study suggests that: (i) The high GCA of the parents can not be taken as a criterion for the evolution of hybrids with high SCA's since the hybrids with high SCA's were associated with respective parents of low GCA's and *vice versa*.

(ii) Since the variances for GCA were usually larger than those for SCA, and since GCA is the result of additive, and SCA non-additive gene effects (Sprague and Tatum, 1942; Fryxel *et al* 1958 and Griffing 1956), the selection of the parental lines on the basis of their GCA's should be given priority over selection on the basis of their SCA's. This conclusion may also be supported from the analysis of variance for general and specific combining ability (Table 15). The results of Table 15 reveal that the variances for GCA were significant except for heading-span at Parkland and for yield per plant at both locations. The variances for SCA were significant only for onset-of-heading, final-heading and plant height (at both locations) and for heading-span and number of tillers per plant (at Parkland). Significance of variances for GCA thus suggests the importance of additive gene effects and emphasizes that substantial differences exist among the parental lines used in the study. (iii) The significant variances for SCA imply that non-additive gene effects for the particular characters are relatively more important and that the hybrids with highest SCA's may be selected for further breeding adaptability tests.

TABLE 16

Mean squares from the analysis of variance of the 5 x 5 F_1 diallel table for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Final heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
a	4	79.1719**	109.6875**	4.1074	4228.0000**	19.3008*	6.1328*	138.7031*	0.2877*	104.8281*	23.5332
		125.8750**	192.2500**	7.8604	4191.0000**	12.7686	8.4102**	91.2188	0.2156*	89.2031**	6.0947
b	10	5.7750	8.5250**	1.4852	68.4000	3.6668	0.6289	28.0187	0.0507	9.0875	11.4297
		6.7125*	21.3812**	13.7445*	67.7000	7.9043	1.5145	13.2562	0.0413	15.7437	2.1000
b_1	1	16.3333	38.1633	5.8800	67.5947	0.7123	0.1574	4.1706	0.0726	10.4398*	15.1135
		20.8033	66.2700	12.4033	31.1918	15.8674	0.5796	3.7705	0.1749	66.0398	2.0817
b_2	4	2.4219	4.4375*	1.8822	112.5625	2.4049	0.7930	14.0703	0.0092	5.3457	5.1953
		4.7959	1.0469	5.1289	93.1719*	13.1418*	1.1104	14.2686	0.0390	8.9922	3.6924
b_3	5	6.3625**	5.8500**	0.2883	33.0125	5.2719	0.5953	43.9750	0.0796	11.8000	15.6836
		5.4500*	28.6750**	20.1060*	54.8625**	2.1195	2.0281	14.3625*	0.0166	11.1000	0.8312
c	4	2.1333	0.6167	1.4333	11.1538	3.8020	0.0725	37.5303	0.0977	11.6772	18.0605
		4.1833	0.5833	2.4667	6.6066	1.9934	0.4659	4.6971	0.0398	14.9461	12.4107
d	6	0.8556	0.8944	0.7111	63.1929*	2.6837	1.9599	19.2044	0.0880*	14.0084	8.6244
		3.5722*	1.1944	2.1056	38.9815**	3.0668	0.4170	7.0210	0.0061	4.3472	7.4908
Blocks x *a*	8	1.0312	0.6328	2.2113	17.7266	4.7915	1.7173	25.6719	0.0542	20.7422	7.8745
		3.5937	4.6406	5.6348	35.6094	4.7622	0.8608	24.4531	0.0572	7.6406	5.7969
Blocks x *b*	20	1.1312	0.6406	0.7294	27.3656	4.9238	2.1734	19.0937	0.0398	8.8656	15.2057
		2.5469	3.6719	5.1647	24.7844	4.9705	0.9705	6.5250	0.0412	10.3906	5.3535
Blocks x b_1	2	9.2467	2.4866	1.5800	77.0164	13.4714	2.2294	42.1510	0.0717	0.4583	47.2437
		8.8466	15.8600	6.2067	270.1160	38.0653	0.0713	6.3986	0.1328	33.9540	1.2041
Blocks x b_2	8	1.0688	0.9307	1.0355	31.9712	4.3863	1.3899	16.3374	0.0487	8.8271	8.9218
		4.0024	1.3726	6.2955	20.4922	1.9459	1.5215	10.4585	0.0377	8.2334	3.0371
Blocks x b_3	10	0.4750	0.3000	0.4725	21.6625	4.9898	3.0066	20.9125	0.0335	10.6437	18.5426
		0.9937	4.6562	4.6720	6.1187	2.8008	0.7113	4.0633	0.0390	10.8035	8.1539
Blocks x *c*	8	0.8333	1.4667	1.0583	16.0278	3.1607	1.2033	12.4407	0.0273	6.5340	8.6371
		2.1833	0.4083	2.1417	24.9243	3.1579	1.3036	17.3466	0.0666	7.7739	8.0467
Blocks x *d*	12	0.6389	1.7444	0.3778	13.0140	1.3007	1.0707	5.8792	0.0293	6.5789	11.2731
		1.0722	1.8944	1.9056	6.9826	1.9370	0.8900	10.4261	0.0204	5.8304	4.4533
Error	48	0.9418	1.0529	0.9433	20.2814	3.7021	1.6601	15.7776	0.0375	9.8848	11.9059
		2.2921	2.8450	3.9244	22.1612	3.5057	0.9876	12.2919	0.0429	8.354	5.6517

*Significant at 5% level
** Significant at 1% level
First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of $(a+b+c+d)$. Each component has been tested against its own block interaction.

Diallel cross analysis

F_1 entries from Appendices III to XXII were sorted out and complete diallel tables were constructed for each replication with respect to all the characters at both locations. All the entries were subjected to Hayman's (1954a) analysis of variance. The results of this analysis are presented in Table 16. In this table component a tests the significance of additive effects and b the dominance effects of genes, while b_1 tests the mean deviations of F_1's from their mid-parent values. The dominance-deviations, if predominantly in one direction, may result in significance of b_1 in an analysis of variance. The component b_2 indicates the extent to which the mean dominance deviations within a given array of the diallel table differ from those of the other arrays. A significant b_2 thus implies that some of the parents contain an excess of dominant alleles. The b_3 component tests the portion of the dominance deviations attributable to individual F_1's. The difference between the reciprocal crosses is assessed by the significance of the c component and maternal effects not ascribable to c are reflected by d. In Table 16 each of the components has been tested for significance against its own block-interaction mean-square. The c was not significantly different from zero at either location for any of the characters studied. Substantial differences among the parents are suggested by the significance of the a component (additive gene effects) for onset-of-heading, final heading, plant height, number of spikeletes per spike and 1000-kernel weight at both locations and number of tillers per plant and number of seeds per spike at Ellerslie. Item b was significant for final heading at both locations and for onset-of-heading and heading-span at Parkland.

TABLE 17

Analysis of variance of W_r-V_r differences for ten characters from F_1 diallel set at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.	F for Entries
Onset-of-heading	9.2560	0.5815	0.1617	3.4689
	18.9050	0.0396	0.2974	0.1332
Final heading	5.1354	1.4540	0.4502	3.2297
	73.2777	11.9745	4.6422	2.5795
Heading-span	0.9138	0.1887	0.1845	1.0227
	31.5321	18.5786	11.9478	1.5550
Plant height	17021.1562	344.3281	200.6953	1.7157
	4453.5938	180.5625	58.2656	3.0990
Number of tillers per plant	37.6399	6.5010	3.5646	1.8238
	9.8287	0.7379	2.0809	0.3546
Number of spikelets per spike	4.3689	0.7859	0.2638	2.9796
	0.5617	0.1118	0.1160	0.9640
Number of seeds per spike	989.3882	83.1030	64.5087	1.2882
	24.4063	23.2917	12.2852	1.8959
Weight of seeds per spike	0.0021	0.0002	0.0003	0.5844
	0.0041	0.0002	0.0002	1.1813
1000-kernel weight	128.4015	7.3713	6.6094	1.1153
	134.1506	21.2359	7.2551	2.9270
Yield per plant	102.4395	13.8542	11.9046	1.1638
	28.0996	5.8340	5.6502	1.0325

First reading under each column refers to Ellerslie and the second to Parkland.

Directional dominance (significance of b_1) was exhibited by 1000-kernel weight at Ellerslie. Significance of b_2 for final heading at Ellerslie and for plant height and number of tillers per plant at Parkland indicates that some parents probably possess more dominant alleles than others for these characters.

The assumptions of no non-allelic interaction, no multiple allelism and uncorrelated parental gene distribution, were checked by analysis of the variance of W_r-V_r. The test of homogeneity of W_r-V_r is given in Table 17. None of the characters showed heterogeneity at either location and the conditions underlying the diallel cross analysis could therefore be accepted as valid. For analysis of the genetic components of variation, the offdiagonal values of the diallel table were replaced with the common mean of the corresponding cross and its reciprocal. The array variances (V_r) and parent-offspring covariances (W_r) over five arrays provided the basis for calculating other second degree statistics which are presented in Table 18. The estimates of genetic components of variation obtained from second degree statistics (Hayman 1954b) are presented in Table 19. Table 18 supplied 35 statistics [(15 V_r's of five arrays and three replications, 15 W_r's, V_{OLO}, W_{OLO1}, V_{OL1}, V_{1L1} and $(M_{L1} - M_{LO})^2$] and 10 constants were fitted to them (5 F_r values, D, H_1, H_2, h and E; F was not considered, as it is the mean of five F_r's), leaving 25 degrees of freedom for error to test the significance of genetic components of variation. The proportional estimates of the genetic parameters from Table 19 for all the characters are given in Table 20. The results shown in Table 19 and 20 supported by the

TABLE 18

Estimates of second degree statistics parameters for ten characters from F_1 diallel set at two locations.

Character	V_{OLO}	W_{OLOI}	V_{OLI}	V_{1LI}	$(M_{LI}-M_{LO})^2$
Onset-of-heading	15.0000	6.2693	2.6367	3.6055	0.8710
	15.7002	7.8816	4.1963	5.3152	1.1096
Final heading	16.9668	7.6781	3.6621	5.0816	2.0354
	27.1514	13.1479	6.4092	9.9770	3.5344
Heading-span	0.5889	0.1901	0.1370	0.3845	0.3136
	3.6111	0.8584	0.2621	2.5528	0.6614
Plant height	486.7744	257.0203	140.9746	152.3508	3.6043
	518.4434	264.6565	139.7002	150.9949	1.6638
Number of tillers per plant	1.4343	0.8816	0.6432	1.2544	0.0379
	5.4749	1.1369	0.4255	1.7429	0.8462
Number of spikelets per spike	1.2283	0.4720	0.2047	0.3093	0.0083
	0.5749	0.3638	0.2805	0.5328	0.0309
Number of seeds per spike	28.9980	11.1666	4.6221	9.2889	0.2224
	12.2275	5.3820	3.0371	5.2459	0.2010
Weight of seeds per spike	0.0384	0.0187	0.0096	0.0180	0.0038
	0.0360	0.0142	0.0072	0.0141	0.0093
1000-kernel weight	16.7744	7.4203	3.4941	5.0057	0.5568
	13.1670	5.8156	2.9736	5.5967	3.5220
Yield per plant	5.4558	1.8886	0.7846	2.6896	0.8060
	0.8875	0.2405	0.2034	0.5532	0.1110

First reading under each column refers to Ellerslie and the second to Parkland.

TABLE 19

Estimates of components of variation
for ten characters from F_1 diallel set at two locations.

Character	D	F	H_1	H_2	h^2	E
Onset-of-heading	14.6845 ± 0.3196**	4.5440 ± 0.7983**	3.5241 ± 0.8630**	3.2439 ± 0.7828**	3.2826 ± 0.5285**	0.3155 ± 0.1305
	14.9359 ± 0.4053**	-1.0433 ± 1.0125	3.4473 ± 1.0946**	2.9471 ± 0.9924**	3.9492 ± 0.6703**	0.7643 ± 0.1655**
Final heading	16.6165 ± 0.5209**	2.8008 ± 1.3011*	5.6702 ± 1.4066**	4.9776 ± 1.2758**	7.9178 ± 0.8614**	0.3503 ± 0.2126
	26.2030 ± 1.0947**	0.5733 ± 2.7346	12.0021 ± 2.9564**	12.3744 ± 2.6815**	13.5304 ± 1.8104**	0.9484 ± 0.4469*
Heading-span	0.2745 ± 0.1321*	0.0402 ± 0.3300	0.5491 ± 0.3568	0.3612 ± 0.3236	1.0532 ± 0.2185**	0.3144 ± 0.0539**
	2.3939 ± 1.1997*	2.2189 ± 2.7495	6.9876 ± 2.9726**	6.5466 ± 2.6962**	1.8088 ± 1.8203	1.3018 ± 0.4494**
Plant height	480.0347 ± 4.6656**	-62.6197 ± 11.6546**	50.5735 ± 12.5999**	32.0255 ± 11.4283**	10.1059 ± 7.7158	6.7396 ± 1.9047**
	511.0740 ± 6.7585**	-30.5825 ± 16.8827	44.6366 ± 18.2521*	30.4400 ± 16.5549	1.9389 ± 11.1770	7.3694 ± 2.7591**
Number of tillers per plant	0.2006 ± 0.5712	-2.1383 ± 1.4269	-0.2819 ± 1.5427	-0.0226 ± 1.3992	-0.6376 ± 0.9447	1.2336 ± 0.2332**
	4.3068 ± 0.3062**	5.005 ± 0.9648**	4.8621 ± 1.0430**	2.9335 ± 0.9460**	2.6375 ± 0.6387**	1.1618 ± 0.1577**
Number of spikelets per spike	0.6753 ± 0.0312**	-0.0951 ± 0.0780	-0.8602 ± 0.0844**	-0.6873 ± 0.0765**	-0.3203 ± 0.0517**	0.5530 ± 0.0128**
	0.2460 ± 0.2050	-0.7193 ± 0.5121	0.3765 ± 0.5536	0.3513 ± 0.5021	-0.0868 ± 0.3399	0.3289 ± 0.0837**
Number of seeds per spike	23.7437 ± 2.5748**	7.0245 ± 6.4318	7.8258 ± 6.9535	8.1585 ± 6.3069	-2.4732 ± 4.2581	5.2543 ± 1.0511**
	8.1325 ± 1.5171**	-1.9871 ± 3.7897	1.0359 ± 4.0970	0.6450 ± 3.7161	-1.8166 ± 2.5089	4.0951 ± 0.6193
Weight of seeds per spike	0.0259 ± 0.0038**	-0.0132 ± 0.0096	0.0031 ± 0.0103	0.0088 ± 0.0096	0.0075 ± 0.0063	0.0125 ± 0.0016**
	0.0217 ± 0.0035**	-0.0021 ± 0.0086	-0.0018 ± 0.0093	-0.0011 ± 0.0085	0.0282 ± 0.0057**	0.0143 ± 0.0014**
1000-kernel weight	13.4832 ± 0.7218**	-0.0819 ± 1.8030	-1.4414 ± 1.9492	-0.5364 ± 1.7680	0.1206 ± 1.1936	3.2912 ± 0.2947**
	10.3857 ± 1.0709**	-0.2660 ± 2.6750	5.0600 ± 2.8920	4.9297 ± 2.6231	12.3080 ± 1.7710**	2.7812 ± 0.4372**
Yield per plant	1.4876 ± 0.2376**	-1.4048 ± 0.5936*	-1.6575 ± 0.6418*	-0.3163 ± 0.5821	0.6845 ± 0.3930	3.9682 ± 0.0970**
	-0.9960 ± 0.2306**	-1.4472 ± 0.5761*	-2.7585 ± 0.6229**	-2.3675 ± 0.5649**	-0.7613 ± 0.3814	1.8834 ± 0.0942**

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
** Significant at 1% level

graphical analysis of regression of W_r upon V_r, lead to the following conclusions:

At both locations, onset-of-heading was inherited as a partially dominant trait, as shown by the mean degree of dominance $[(H_1 \div D)^{1/2} = 0.48]$ and regression line (b_{W_r/V_r}) which passes above the origin (Figure 1). The proportion of genes with positive and negative effects in the parents $[H_2 \div 4H_1]$ is 0.23 at Ellerslie and 0.21 at Parkland, suggesting a slight asymmetry of alleles at the loci exhibiting dominance. The proportion of dominant to recessive genes in the parents $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ is 1.92 at Ellerslie and 0.86 at Parkland, suggesting a preponderance of dominant genes in the parents at Ellerslie and equal proportions of dominant and recessive genes at Parkland. The coefficient of correlation between the parental order of dominance, i.e. $(W_r + V_r)$ and the parental measurements $[(Y_r)$; the corresponding values of the main diagonal of the diallel table] are 0.97 and 0.66 at Ellerslie and Parkland respectively. High positive correlation at both locations suggests an association between recessive genes with late heading and dominant genes contributing towards early heading. This situation is reflected in the standardized deviation graph (Figure 2) where all the Y_r, $(W_r + V_r)$ parental intercepts occupy (+,+) and (-,-) quadrants, except Khush-hal at Parkland. Figure 1 classifies Marquis as the highly recessive and Inia as the highly dominant parents at both locations, since they lie, respectively, farthest and nearest to the point of intersect of regression line and limiting parabola. Figure 2 supplements this conclusion by revealing

TABLE 20

Proportional values of the estimates of genetic parameters for ten characters from F_1 diallel set at two locations.

Character	$[H_1 + D]^{1/2}$	$[H_2 + 4H_1]$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}\right]$	h^2/H_2	r_{Y_r, W_r+V_r}	Heritability
Onset-of-heading	0.4899*	0.2301*	1.9232*	1.0119*	0.9742	0.9837
	0.4804*	0.2137*	0.8645*	1.3400*	0.6627	0.6642
Final heading	0.5842*	0.2195*	1.3372*	1.5907*	0.9712	0.7955
	0.6768*	0.2578*	1.0329*	1.0934*	0.9661	0.6325
Heading-span	1.4144	0.1644	1.1093	2.9160	0.1322	0.1344
	1.7419*	0.2342*	1.7646 †	0.2763	0.7382	0.1875
Plant height	0.3246*	0.1583*	0.6654*	0.3156	0.1720	0.7740
	0.2955*	0.1705*	0.8161†	0.0637	0.0770	0.8299
Number of tillers per plant	1.1855	0.0200	-0.6361	28.1984	0.8341	0.0281
	1.0625*	0.1508*	3.4090*	0.8991*	0.8924	0.4885
Number of spikelets per spike	1.1286*	0.1997*	0.8826†	0.4661*	-0.2485	0.3182
	1.2370	0.2333	-0.0833	-0.2472	0.7543	0.0925
Number of seeds per spike	0.5741*	0.2606	1.6942	-0.3031	-0.3653	0.5211
	0.3569	0.1557	0.4900	-2.8162	-0.0519	0.2953
Weight of seeds per spike	0.3484	0.7000	0.1561	0.8524	-1.1500	0.2809
	0.2912	0.1445	0.7188	-26.4099	-0.8890	0.2739
1000-kernel weight	0.3270	0.0930	0.9816	-0.2248	-0.7287	0.5331
	0.6980	0.2436	0.9640	2.4967	-0.9252	0.3869
Yield per plant	1.0556	0.0477	0.3819	-2.1646	-0.0082	0.0869
	1.6642	0.2146	0.3922	0.3216	-0.8646	-0.1905

First reading under each column refers to Ellerslie and second to Parkland.
*Genetic component of variation for characters significantly different from zero at $P \leq 0.05$.
†Components D and H_1 significant, F non-significant ($P > 0.05$).

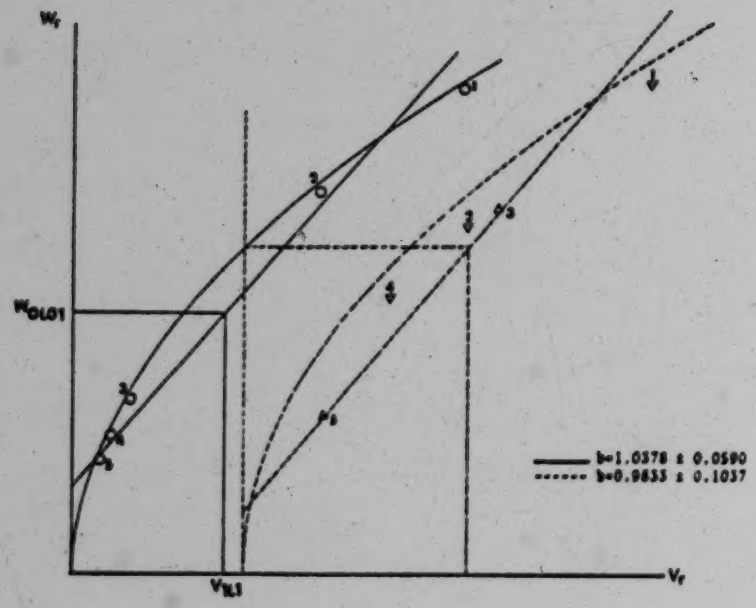

Figure 1. W_r, V_r graph for onset-of- heading from F_1 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

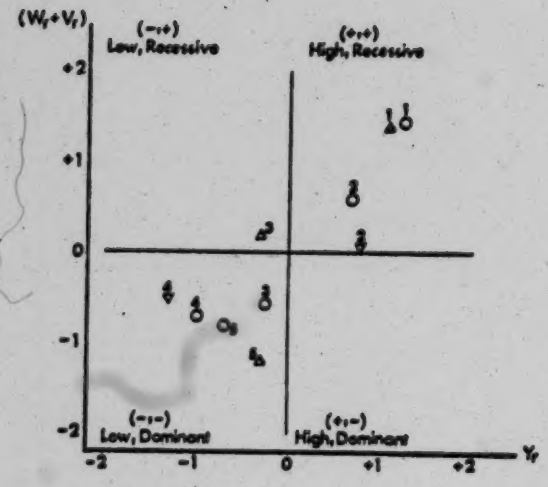

Figure 2. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from F_1 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

that at both locations the highly recessive parent contributes towards late heading (+,+ quadrant) and the highly dominant one towards early heading (-,- quadrant). As far as other parents are concerned, Chinook and Ciano, lying in (+,+) and (-,-) quadrants, may be classified as recessive late headers and dominant early headers. Khush-hal's order of dominance seems to be affected by the environmental influence, being a dominant early header at Ellerslie (-,- quadrant) and a recessive medium-early header (-,+ quadrant) at Parkland. The number of groups of genes $(h^2/H_2) \simeq 1$ at both locations, suggests that at least one group of genes control onset-of-heading and exhibit dominance. The heritability estimates of 98.37% at Ellerlie and 66.42% at Parkland show that the character is highly heritable.

The results from Table 19 and 20 for final heading (Figures 3, 4) and heding-span (Figures 5,6) are subject to the same kind of interpretation as for onset-of-heading except for changes in the relative positions of the parents with respect to their ranking order for dominance, and therefore they are not discussed separately.

For plant height, the mean degree of dominance of 0.3 at both locations shows that height is inherited as a partially dominant character. The W_r, V_r graph (Figure 7) with a regression line intersecting the limiting parabola above its origin supports the above conclusion . The proportion of genes with positive and negative effects in the parents is approximately the same for both locations (0.158 at Ellerslie and 0.170 at Parkland), indicating asymmetry in the distribution of alleles at loci exhibiting dominance. The ratio of dominant to recessive

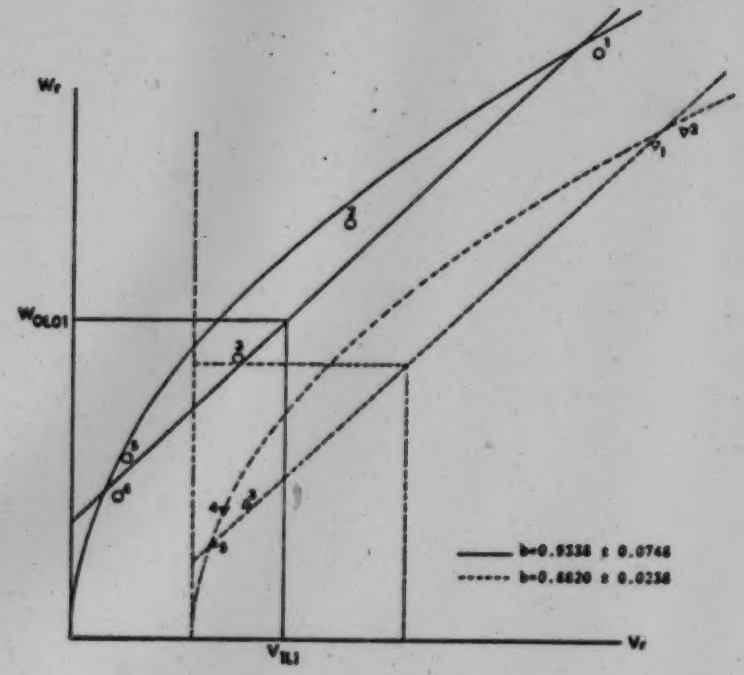

Figure 3. W_r, V_r graph for final heading from F_1 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

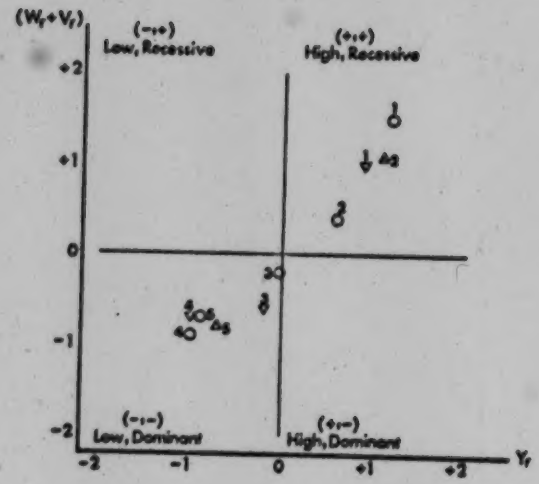

Figure 4. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from F_1 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

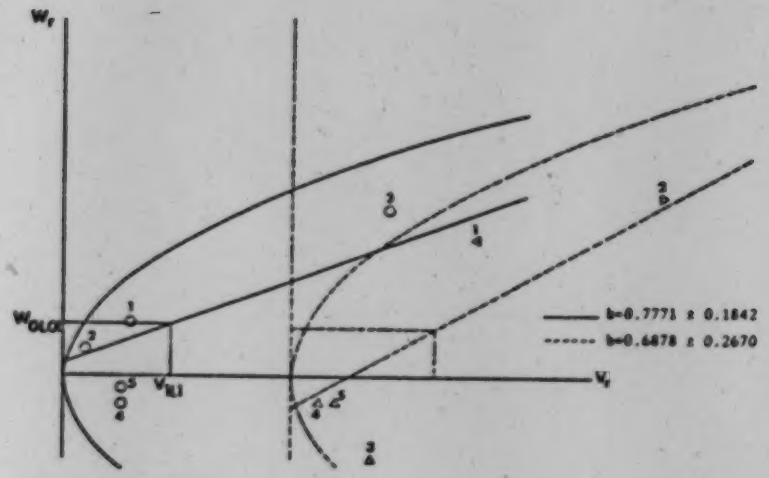

Figure 5. W_r, V_r graph for heading-span from F_1 diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

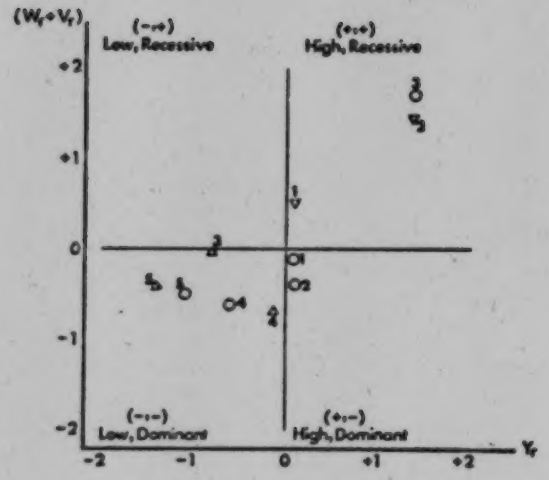

Figure 6. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from F_1 diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

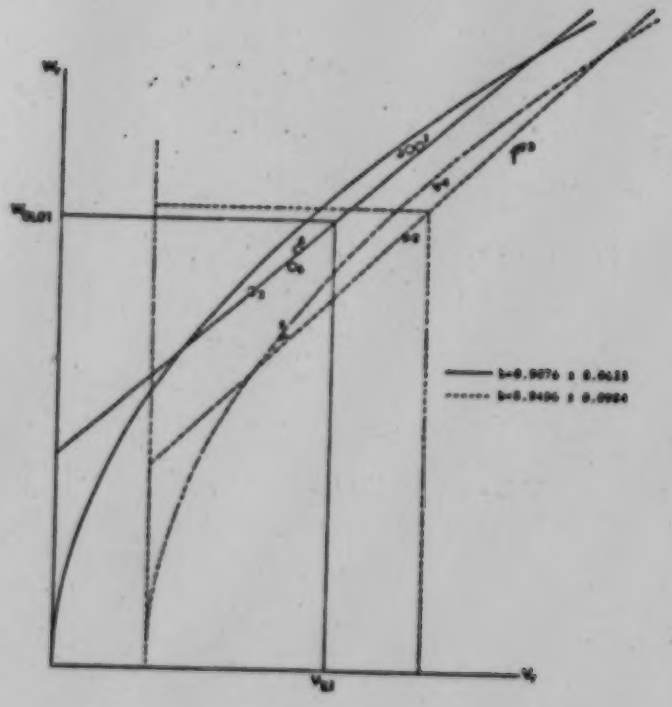

Figure 7. W_r, V_r graph for plant height from F_1 diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

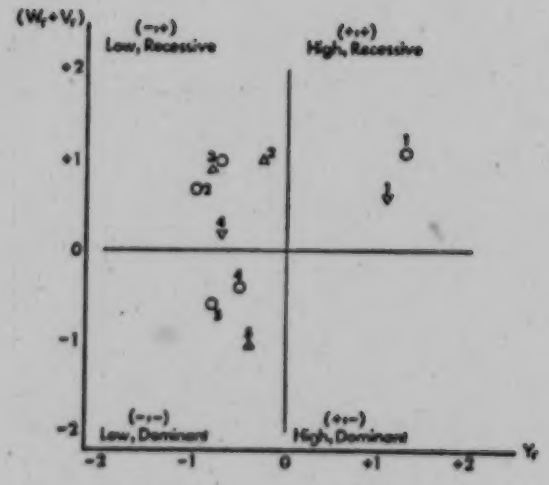

Figure 8. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from F_1 diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

genes in the parents is approximately equal to one at both locations, suggesting that the parents contain equal numbers of dominant and recessive genes. The coefficient of correlation between the parental order of dominance and parental measurements is 0.17 at Ellerslie and 0.07 at Parkland, indicating weak association between the measurements of the parents and their order of dominance. Figure 7 indicates that Marquis at Ellerslie and Khush-hal at Parkland are the most recessive parents while Inia at both the locations is the most dominant parent. Figure 8 classifies the parental order of dominance together with their height performance. It places highly recessive parents Marquis (at Ellerslie) and Khush-hal (at Parkland) into (+,+) and (-,+) quadrants, showing that recessiveness of the former is responsible for tallness, while the recessive genes of the latter carry effects decreasing height. The position of Inia in the (-,-) quadrant of the graph (Figure 8) at both locations suggests that it contains a preponderance of dominant genes contributing towards shortness. The ranking order of Ciano appears to be influenced by location effects. At Ellerslie, it is highly dominant, contributing towards reduced height while at Parkland it has an excess of recessive genes, again responsible for shortness. The character seems to be consistently highly heritable over the locations (77.40% heritability at Ellerslie and 82.99% at Parkland).

The genetic components of variation, D, F, H_1 and H_2 are not significant for number of tillers per plant at Ellerslie and therefore estimates of mean degree of dominance, proportion of dominant to

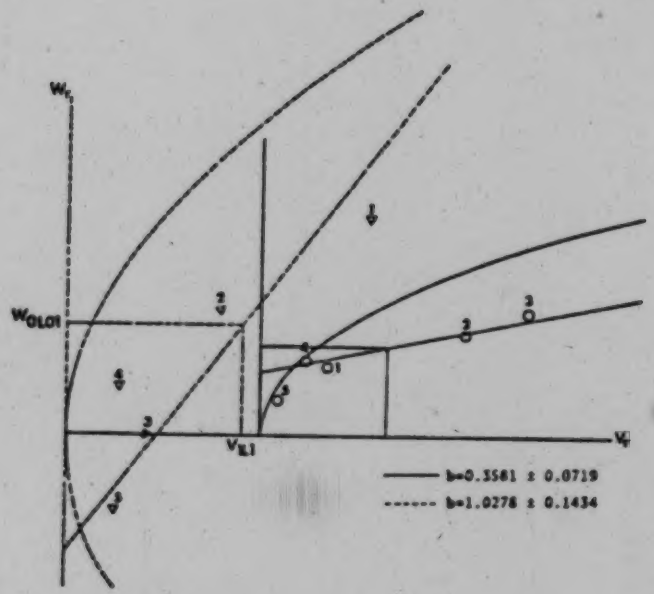

Figure 9. W_r, V_r graph for number of tillers per plant from F_1 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

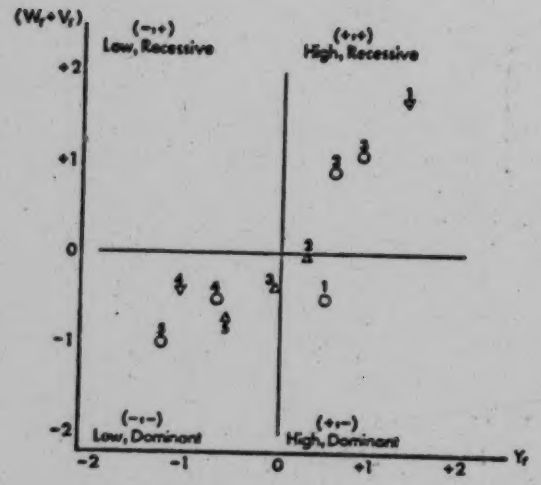

Figure 10. Standardized deviation graph of $[Y_r]$ $[W_r + V_r]$ for number of tillers per plant from F_1 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

recessive genes in the parents etc. should be meaningless (as suggested by Hayman, 1954b). Moreover, the W_r, V_r graph (Figure 9) for Ellerslie is distorted. The mean degree of dominance at Parkland (1.06) indicates over-dominance. This is supported by Figure 9 in which the regression line intersects the limiting parabola above its origin. The proportion of genes with negative and positive alleles at loci exhibiting dominance is 0.15 revealing asymmetry in distribution of alleles. The proportion of dominant to recessive genes in the parents is 3.409 which indicates an excess of dominant genes in the parents. Consequently Khush-hal, Ciano and Inia are categorized as parents with a preponderance of dominant genes, and of these Inia is the most dominant one as it lies closest to the point of intersection of the regression line with the limiting parabola (Figure 9). The significant positive correlation between the parental order of dominance and the parental measurements (0.80) shows that the genes with negative effects for number of tillers per plant are mostly dominant and those with positive effects are mostly recessive. This is shown graphically in Figure 10 where parental Y_r, $(W_r + V_r)$ intercepts occupy only the (+,+) and (-,-) quadrants. Ciano and Inia contain an excess of dominant genes (-,- quadrant) with lower tillering capacity. Chinook appears to be recessive, with a higher number of tillers per plant at Ellerslie, but shows an equal number of recessive and dominant genes at Parkland. Marquis and Khush-hal appear to be inconsistent with respect to order of dominance. At Ellerslie, Marquis has an excess of dominant genes but at Parkland it has become highly recessive. The reverse situation exists with Khush-hal which is placed in the (+,+)

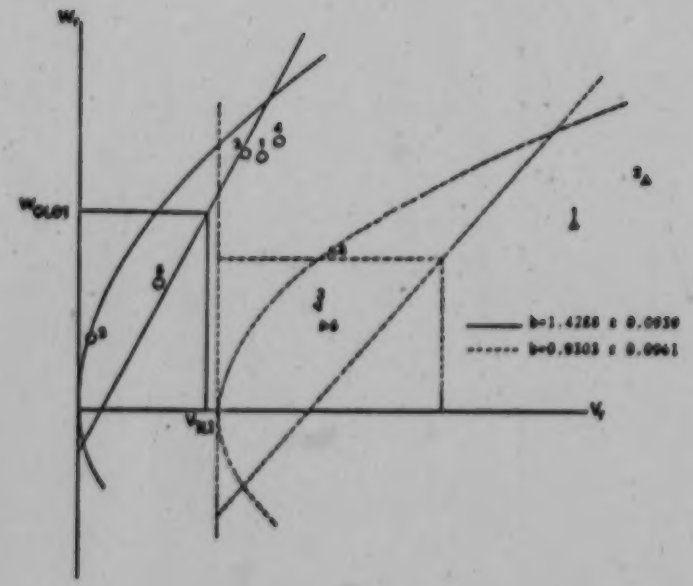

Figure 11. W_r, V_r graph for number of spikelets per spike from F_1 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

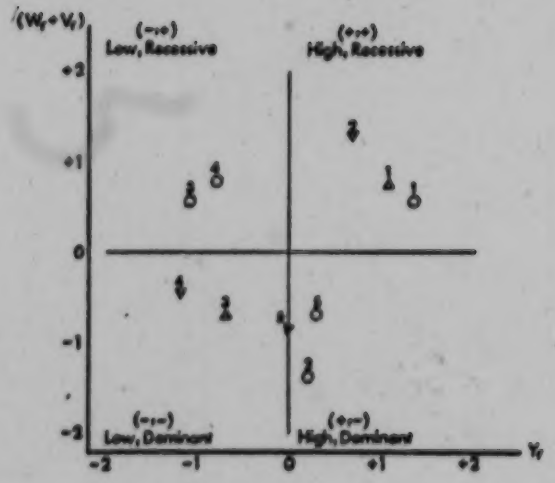

Figure 12. Standardized deviation graphs of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from F_1 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

quadrant at Ellerslie and in the (-,-) quadrant at Parkland. The estimate for the number of groups of genes controlling tiller number seems to be questionable for Ellerslie (Table 20) where the relevant components of variation were nonsignificant (Table 19). However it is approximately equal to one at Parkland, showing that at least one group of genes exhibiting dominance controls tillering. The heritability of this character, low at Ellerslie (2.86%) and relatively high at Parkland (48.85%) seems to be affected by environmental differences.

With regard to number of spikelets per spike, there was over-dominance at both locations, since $[H_1/D]^{1/2} > 1$ and the W_r/V_r regression line intersects the limiting parabola below its origin (Figure 11). The genetic components of variation were not significant for Parkland and the proportional estimates of genetic parameters given in Table 20 have therefore to be ignored. For Ellerslie, the proportion of genes with positive and negative alleles at loci exhibiting dominance is approximately 0.2, indicating a slight asymmetry in distribution. The proportion of dominant to recessive genes in the parents is 0.99, suggesting approximately equal proportions of dominant and recessive genes. Figure 11 classifies Marquis, Khush-hal and Ciano as having an excess of recessive genes. The correlation coefficient $(r_{Y_r}, W_r + V_r)$ of -0.2 at Ellerslie suggests that parental measurements are not related with their order of dominance, while $r = 0.75$ at Parkland suggests that genes for lower spikelet number per spike are dominant. Order of dominance of the parents (Figure 12) seems to be inconsistent for the two locations except Marquis and Inia. Chinook, the highly recessive parent at Parkland

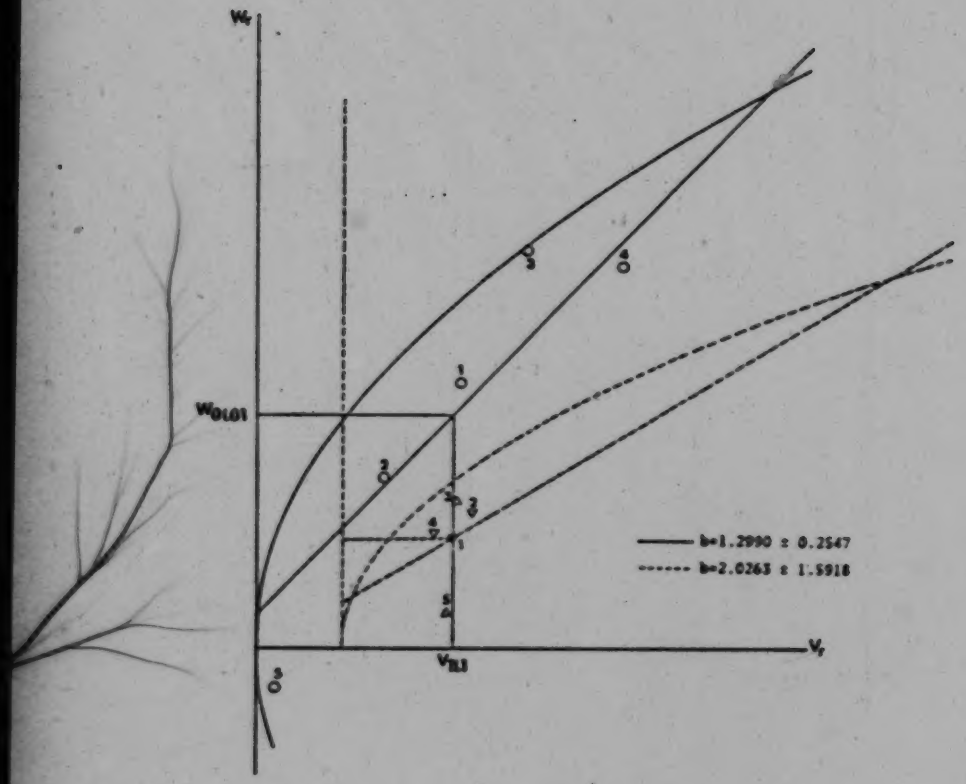

Figure 13. W_r, V_r graph for number of seeds per spike from F_1 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

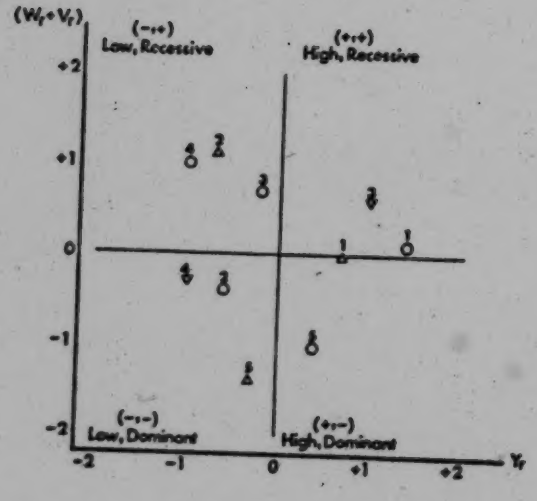

Figure 14. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from F_1 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

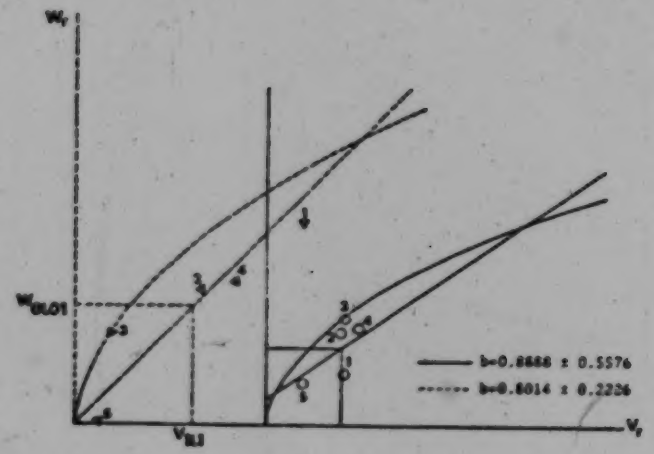

Figure 15. W_r, V_r graph for weight of seeds per spike from F_1 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

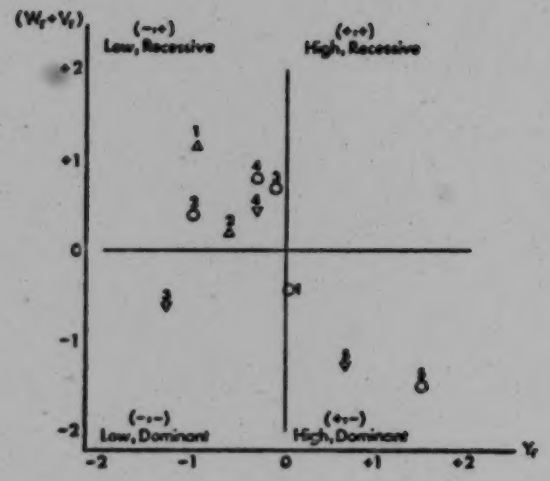

Figure 16. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from F_1 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

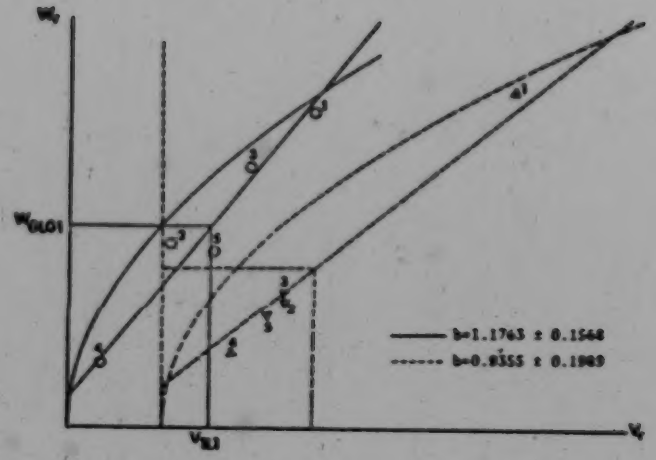

Figure 17. W_r, V_r graph for 1000-kernel weight from F_1 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Ellerslie

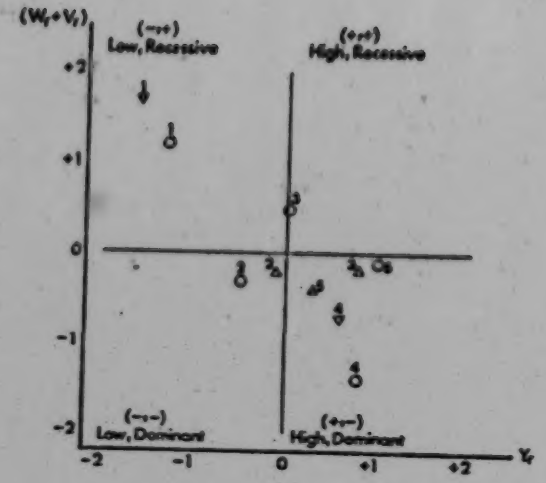

Figure 18. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from F_1 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

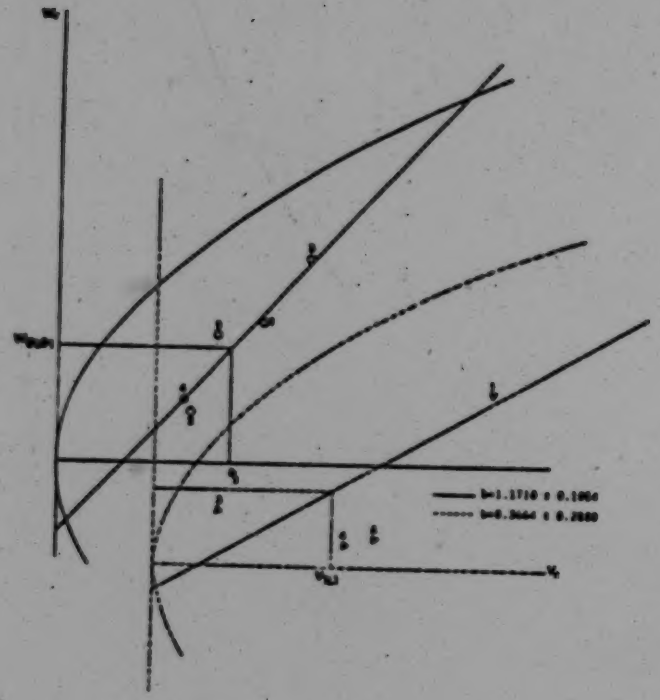

Figure 19. W_r, V_r graph for yield per plant from F_1 diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

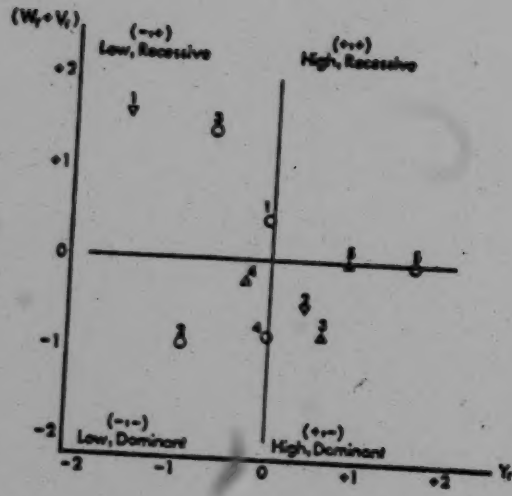

Figure 20. Standardized deviation graph of [Y_r] and [W_r + V_r] for yield per plant from F_1 diallel set.

o = Y_r, [W_r + V_r] intercepts at Ellerslie

Δ = Y_r, [W_r + V_r] intercepts at Parkland

appeared highly dominant at Ellerslie. Khush-hal and Ciano with a preponderance of recessive genes at Ellerslie (-,+ quadrant) contained mostly dominant genes at Parkland (-,- quadrant). The ratio $h^2/H_2 = 0.46$ suggests that possibly one group of dominant genes is controlling the number of spikelets per spike. Heritability estimates of 31.82% at Ellerslie and 9.25% at Parkland suggest that not only the character is low heritable but inconsistent over the locations also.

As far as the other components of yield i.e. number of seeds per spike (Table 19, 20 and Figure 13, 14), weight of seeds per spike (Table 19, 20 and Figure 15, 16) and 1000-kernel weight (Table 19, 20 and Figure 17, 18) are concerned, the interpretation of the results from relevant tables and figures will be similar. The changes in the relative positions of the parents for their order of dominance may be encountered which may be interpreted accordingly.

The results of diallel cross analysis for yield per plant are meaningless both for Ellerslie and Parkland data. Paradoxically, H_1 for Ellerslie and D, H_1 and H_2 for Parkland have negative values significantly different from zero. Consequently the V_r, W_r graph (Figure 19) for Parkland appears to be severely distorted. The respective graph for Ellerslie does not seem to be distorted and suggests the validity of the hypotheses underlying the diallel analysis. However, a significant negative H_1 invalidates the interpretation of the graph. The same objection applies to standardized deviation graph (Figure 20) also.

ANALYSIS OF F_2 DATA

It will not be out of place to mention again that the F_2 generation hybrids were duplicated in each replication at both locations,

TABLE 21

Simple correlation coefficients between ten characters from F_2 diallel set at two locations.

Character	1	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	-	0.382** 0.831**	0.115 -0.040	0.763** 0.798**	0.196 0.522**	0.433** 0.536**	0.275* 0.306**	-0.274* -0.400**	-0.610** -0.686**	-0.249* -0.126
2. Final heading		-	0.025 0.522**	0.253* 0.750**	0.176 0.556**	0.142 0.516**	0.087 0.234*	-0.114 -0.398**	-0.229* -0.638**	-0.021 -0.089
3. Heading-span			-	0.302** 0.122	0.166 0.205	0.027 0.102	-0.074 -0.049	-0.299** -0.102	-0.322** -0.095	-0.201 0.037
4. Plant height				-	0.394** 0.506**	0.575** 0.652**	0.263* 0.248*	-0.287* -0.412**	-0.633** -0.687**	0.009 -0.034
5. Number of tillers per plant					-	0.204 0.353**	0.081 0.060	-0.032 -0.278*	-0.113 -0.505**	0.565** 0.238*
6. Number of spikelets per spike						-	0.625** 0.444**	0.218 0.192	-0.346** -0.349**	0.267* 0.329**
7. Number of seeds per spike							-	0.657** 0.160	-0.130 -0.141	0.259* 0.065
8. Weight of seeds per spike								-	0.650** 0.701**	0.392** 0.473**
9. 1000-kernel weight									-	0.252* 0.265*
10. Yield per plant										-

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
**Significant at 1% level

partly to meet the entry requirements of the partially balanced lattice design, and partly to reduce the genetic sampling error inherent in the segregating generation. Though the heading data and yield observations were recorded separately for the two repetitions, the analysis of the data is based on their average.

Simple correlation coefficients for all the characters are shown in Table 21. The results reveal that:

Onset-of-heading was positively correlated with final heading, plant height, number of spikelets per spike, number of seeds per spike, and negatively correlated with weight of seeds per spike, 1000-kernel weight and yield per plant at both locations. Correlation with number of tillers per plant was only exhibited at Parkland. The negative association of onset-of-heading with yield and its two components, weight of seeds per spike and 1000-kernel weight, suggests that early maturing varieties are higher yielders and consequently their seed weighs more than the late maturing ones. This kind of relationship was also noticed for F_1 hybrids. Correlation of final heading and heading-span with other characters has the same kind of interpretation.

Plant height exhibited significant positive correlation with number of tillers per plant, number of spikelets per spike, number of seeds per spike and 1000-kernel weight at both locations. Correlation with yield per plant was not significant.

Number of tillers per plant exhibited positive correlation with yield per plant at both locations and with number of spikelets per spike at Parkland but was negatively associated with weight of seeds per

TABLE 22

Varimax rotated factor matrix for ten characters from F_2 diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.977	0.958	0.149	-0.047	-0.178	-0.055
	0.886	0.896	0.023	0.253	-0.116	-0.075
Final heading	0.981	0.095	0.129	-0.029	-0.208	0.346
	0.940	0.794	0.001	0.252	-0.090	0.488
Heading-span	0.996	0.152	-0.051	0.009	-0.140	0.975
	0.993	0.050	-0.036	0.071	0.019	0.992
Plant height	0.851	0.746	0.267	0.250	-0.372	0.148
	0.889	0.922	0.012	0.194	-0.004	0.049
Number of tillers per plant	0.912	0.277	-0.039	0.903	-0.006	0.133
	0.917	0.351	0.013	0.848	0.235	0.142
Number of spikelets per spike	0.834	0.288	0.811	0.162	-0.257	-0.022
	0.883	0.688	0.590	0.046	0.233	0.071
Number of seeds per spike	0.903	0.186	0.904	0.039	0.221	-0.014
	0.981	0.156	0.967	0.098	0.049	-0.050
Weight of seeds per spike	0.994	-0.234	0.581	0.082	0.760	-0.129
	0.943	-0.381	0.725	-0.346	0.391	-0.024
1000-kernel weight	0.913	-0.462	-0.155	0.072	0.802	-0.162
	0.880	-0.625	0.059	-0.546	0.411	-0.005
Yield per plant	0.898	-0.285	0.278	0.839	0.105	-0.156
	0.929	-0.045	0.252	0.129	0.920	0.008
% of total variability explained	92.590	28.424	20.287	16.261	15.814	11.805
	92.399	34.420	18.768	13.540	13.089	12.581

First reading under each column refers to Ellerslie and second to Parkland

spike and 1000-kernel weight at Parkland. Negative correlations with weight of seeds per spike and 1000-kernel weight establish an inverse relationship indicating that more the tillers per plant, the higher is the yield and the lower the weight of seeds per spike and 1000-kernel weight. The correlation coefficients of other components of yield, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight may be explained in the same manner.

Yield per plant was positively correlated with its components, viz., number of tillers per plant, number of spikelets per spike, weight of seeds per spike and 1000-kernel weight. It was negatively associated with onset-of-heading at Ellerslie, while its correlation at Parkland was not significant. Negative correlation of yield with onset-of-heading indicates that high yielding varieties are usually early maturing.

Factor analysis was performed on the complete F_2 diallel data. Four principal factors, derived by factorizing correlation matrix into a varimax rotated factor matrix, accounted for 81.7% of the variability present in the data. Since it was thought that 82% of the variation (as explained by these four factors) was not sufficient, the number of factors was raised to five and the procedure was repeated through computerization. The five factors were found to explain 92% of the variation in the data. A further six factor matrix explained 96% of the variability, it was not significantly different from the five factor-matrix which was therefore considered and the results are given in Table 22.

Since the first factor showed the highest loadings for

onset-of-heading and final heading at both locations and accounted for 28% of variability at Ellerslie and 34% at Parkland, it was named *lateness*. It was positively affected by plant height and negatively by weight of seed per spike, 1000-kernel weight and yield per plant at both locations. This implies that a longer heading period causes the plants to grow taller but yield less, with lower seed weight per spike and consequently lower 1000-kernel weight. Number of tillers per plant, number of spikelets per spike and number of seeds per spike at both locations contributed very little to this factor.

The second principal component was termed *yield-components*. Although earlier the term *yielding-capacity* was applied in the F_1 factor analysis, the above term is considered more suitable because of the consistently higher loadings for yield components. Thus this component shows maximum loadings for number of spikelets per spike, number of seeds per spike and weight of seeds per spike at both locations. Negative contributions towards this factor due to heading-span at both locations and number of tillers per plant and 1000-kernel weight at Ellerslie reveal that varieties with longer maturing times yield less, produce fewer tillers per plant and show lower 1000-kernel weight.

The third principal component was named *tillering-capacity* as it provided the maximum contribution to number of tillers per plant at both locations. The factor accounted for 16% and 13.5% of the total variability in the data at Ellerslie and Parkland respectively. Yield was significantly affected at Ellerlie, but at Parkland, the contribution towards yield was comparatively low. Number of spikelets per spike,

TABLE 23

Estimates of general combining ability of five parental lines used in F_2 diallel set for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.8000	1.3167	-0.3667	-1.6833	-1.0667
	2.2267	2.0267	-1.0900	-2.0066	-1.1566
Final heading	1.9767	1.5767	-0.0733	-1.9733	-1.5066
	2.0334	2.5667	-0.9167	-2.0333	-1.6570
Heading-span	0.1500	0.3667	0.2667	-0.3167	-0.4667
	-0.2033	0.5467	0.1800	-0.0367	-0.4867
Plant height	13.3708	10.0921	-6.7329	-7.3467	-9.3831
	12.9692	12.0445	-7.7827	-9.2980	-8.9530
Number of tillers per plant	-0.0055	0.4139	0.4435	-0.2707	-0.8512
	0.8860	0.6827	0.5310	-0.9973	-1.1023
Number of spikelets per spike	0.7264	0.2257	-0.6356	-0.4576	0.1412
	0.6867	0.4672	-0.3060	-0.7084	-0.1394
Number of seeds per spike	3.1883	-1.5763	-1.7061	-2.1989	2.2930
	2.2384	-1.1155	0.2738	-2.4832	1.0865
Weight of seeds per spike	0.0283	-0.1592	-0.0475	-0.0079	0.1863
	-0.0274	-0.1023	+0.0665	-0.0431	0.1063
1000-kernel weight	-2.0321	-2.2150	0.4223	1.7856	2.0392
	-2.2536	-1.3656	1.2445	1.2144	1.1603
Yield per plant	0.0508	-1.4712	-0.7275	0.6961	1.4518
	-0.5307	0.1256	0.6319	-0.5374	0.3109

First reading under each column refers to Ellerslie and second to Parkland.

number of seeds per spike and heading-span at both locations , weight of seeds per spike and 1000-kernel weight at Ellerslie contributed positively to this factor.

The fourth principal factor, accounting for 15% and 13% variability at Ellerslie and Parkland and carrying the highest loadings for 1000-kernel weight at both locations, was called *kernel-weight*. The factor was contributed to by weight of seeds per spike and yield per plant at both locations, although the effect of number of seeds per spike appears to be slight. Other characters such as plant height, final heading and onset-of-heading at both locations were negatively affected.

The fifth principal factor, since it was termed *heading period*, was strongly affected by heading-span. It explained 12% of the total variation at both locations, and was adversely affected by yield and its components. Final heading, plant height and number of tillers per plant at both locations scored positively for this factor but their contribution was relatively low.

Combining ability analysis

Estimates of general combining ability for the five parental lines are presented in Table 23. Marquis scored highest for onset-of-heading and Ciano lowest at both locations. The same was true for final heading. For heading-span, Chinook ranked first and Ciano last. In plant height, Marquis excelled at both locations while Inia at Ellerslie and Ciano at Parkland were lowest. For number of tillers per plant, Khush-hal ranked first at Ellerslie and Chinook ranked first at Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_2 diallel set at two locations.

TABLE 24 Onset-of-heading

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	-0.0500	-1.1166	-0.7166	-0.9166	1.8000	3.1762	-0.1594
			1.2066	-0.2600	-1.5100	-1.1100	2.2267	4.8224	-0.3394
Chinook		-0.3333	-	-0.4667	-0.7333	-0.5167	1.3167	1.6699	-0.1586
		0.1667		-0.6434	0.1900	-1.8267	2.0267	3.9718	0.1459
Khush-hal		-0.4167	-0.4167	-	0.1167	0.3334	-0.3667	0.0707	0.3288
		-0.4167	0.1667		-0.3600	-1.0434	-1.0900	1.0522	-1.1789
Ciano		0.0	0.8333*	0.3333	-	0.5667	-1.6833	2.7697	0.1956
		-0.4167	0.2500	-0.2500		1.2066	-2.0066	3.8908	0.4759
Inia		0.0833	0.6667	0.3333	0.4167	-	-1.0067	1.0740	0.3537
		-0.6667	-0.0833	-0.2500	-0.4167		-1.1556	1.2020	2.0317

Reciprocal effects

TABLE 25 Final heading

Marquis		-	0.2233	-1.1267	-0.6434	-1.0267	1.9767	3.8498	-0.1441
			1.0167	-1.3833	-1.4333	-1.2333	2.0334	3.9308	-0.5093
Chinook		-0.0833	-	0.3566	-1.0767	-0.2100	1.5767	2.4284	-0.1275
		0.5833		-1.8333	-0.8000	-1.6833	2.5667	6.3842	-0.0158
Khush-hal		-0.0833	-0.6667	-	-0.3434	-0.5600	-0.0733	-0.0523	0.3214
		0.3333	0.2500		0.5167	0.3000	-0.9167	0.6366	1.2490
Ciano		-0.6667	0.6667	0.4167	-	1.2567	-1.9733	3.8362	0.4196
		-0.1667	-0.3333	-0.6667		1.0833	-2.0333	3.9306	0.4779
Inia		0.7500*	0.6667	0.3333	0.4167	-	-1.5066	2.2123	0.8529
		-0.0833		0.3333	-0.6667		-1.6500	2.5188	1.3635

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances of genoral and specific combining ability from F_2 diallel set at two locations.

TABLE 26. Heading-span

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.1667	0.0167	0.1000	-0.0833	0.1500	-0.0443	-0.1671
			0.0200	-1.1133	0.0200	-0.1133	-0.2033	-0.2013	-0.6067
Chinook		0.2500	-	0.7167	-0.4500	0.2000	0.3667	0.0676	-0.1578
		0.4167		-1.1967	-0.9800	0.1367	0.5467	0.0562	-0.6065
Khush-hal		0.3333	-0.2500	-	-0.4333	-0.8667	0.2667	0.0043	0.0042
		0.7500	0.0833		0.8867	1.3367	0.1800	-0.2103	0.2838
Ciano		-0.6667	-0.1667	0.0833	-	0.7167	-0.3167	0.0334	-0.0337
		0.3333	-0.5833	-0.4167		-0.1133	-0.0367	-0.2413	-0.0243
Inia		0.6667	0.0	0.0	0.0	-	-0.4667	0.1509	0.2701
		0.5833	0.2500	0.5833	-0.2500		-0.4867	-0.0058	0.0037

Reciprocal effects

TABLE 27. Plant height

Marquis		-	2.8015	0.0336	-1.9122	-5.2829	13.3708	177.5788	-2.9988
			1.8702	5.4357	-1.9114	-6.1106	12.9892	166.6538	-5.1606
Chinook		-1.1342	-	1.3486	-3.5393	2.7586	10.0921	100.6507	-0.9129
		2.0642		1.2654	-1.3834	0.2390	13.0445	168.0942	-3.9947
Khush-hal		3.3558*	1.7808	-	1.3133	-0.2195	-6.7329	44.1325	-2.3549
		0.8525	3.4392		0.1846	-2.8154	-7.7827	58.5057	5.2222
Ciano		-0.8783	3.8492*	0.0467	-	1.0260	-7.3467	52.7748	2.9703
		0.0633	5.0650*	0.0592		1.3933	-9.2980	84.3886	-3.2934
Inia		12.9255**	5.8667**	-0.2958	1.5775	-	-9.3831	86.8439	9.5876
		8.2025**	5.3258*	-0.4642	-0.7742		-8.9530	78.0926	10.5941

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.
* Significant at 1% level
**Significant at 5% level

For number of spikelets per spike, Marquis was highest at both locations while Khush-hal at Ellerslie and Ciano at Parkland ranked lowest. For number of seeds per spike, Marquis ranked highest at both locations and Ciano was the lowest. For weight of seeds per spike and 1000-kernel weight, Inia ranked first at both locations, while Chinook ranked last for weight of seeds per spike; and for 1000-kernel weight, Marquis at Parkland and Chinook at Ellerslie ranked last. For yield, Inia at Ellerslie and Khush-hal at Parkland scored highest GCA and Khush-hal at Ellerslie and Ciano at Parkland ranked lowest.

Specific combining abilities of the F_2 hybrids, the reciprocal effects and the variances for general and specific combining abilities are given in Tables 24 to 33. These are discussed under individual characters.

Cross (CxI) had the highest SCA for onset-of-heading (Table 24) at both locations and (MxK) at Ellerslie and (MxI) at Parkland were the lowest. Hybrid (CxI) with the highest SCA had parents with the lowest GCA's at both locations. Similarly the lowest ranking hybrids (MxK) and (MxI) had one parent (Marquis) with the highest GCA at both locations. These kinds of results support those of the F_1 combining ability analyses. Thus it is seen that parental lines with high GCA's do not necessarily produce hybrids with high SCA's. The variances for GCA were usually larger than those for SCA except for Khush-hal at Ellerslie and Inia at Parkland. Relatively high SCA variances for Inia and Khush-hal imply an inconsistency in their SCA performance of their hybrids at both locations. Reciprocal effects were generally non-significant except for (CxCH) at Ellerslie which may be ascribed to the female parent of the hybrid.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_2 diallel set at two locations.

TABLE 28. Number of tillers per plant

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.0155	-0.5067	0.05200	0.0377	-0.0055	-0.1858	-0.4646
			-0.7810	-0.5043	-0.6510	-0.3043	0.8860	0.5798	-0.5129
Chinook		-0.0833	-	0.4832	-0.9860	0.7246	0.7246	0.4139	-0.4646
		-0.3583		0.9407	-0.2310	-0.2427	0.6027	0.2609	-0.3096
Khush-hal		0.7260	0.5167	-	0.8520	-0.7987	0.4435	0.0108	-0.3012
		-1.0667	0.1750		-0.2043	0.1827	0.5310	0.0768	-0.1332
Ciano		-0.4185	0.3667	0.5158	-	0.7167	-0.2707	-0.1126	0.1023
		0.6250	0.8583	-0.0167		0.3123	-0.9973	0.7895	-0.3400
Inia		0.8230	0.7500	0.2437	0.4908	-	-0.5812	0.1520	0.0947
		0.0667	0.1250	0.0333	-0.0500		-1.1023	1.0100	-0.4188

Reciprocal effects

TABLE 29. Number of spikelets per spike

Marquis		-	-0.0184	0.3592	-0.2315	-0.0934	0.7264	0.4810	-0.1169
			0.5606	0.1479	0.1164	-0.1162	0.6867	0.4044	-0.1677
Chinook		0.8083*	-	-0.0646	-0.1672	0.5422	0.2257	0.0042	-0.1168
		0.0222		0.4920	-0.3278	-0.1107	0.4672	0.1512	-0.0629
Khush-hal		-0.2523	-0.0500	-	0.3346	-0.5709	-0.6356	0.3537	-0.0725
		-0.0472	0.3832		-0.3072	-0.1203	-0.3060	0.0266	-0.0796
Ciano		-0.0117	0.1972	0.2123	-	0.1788	-0.4576	0.1626	-0.0524
		-0.0870	-0.2613	0.2750		0.2484	-0.7084	0.4348	-0.0959
Inia		0.4678	0.1057	-0.3203	-0.1243	-	0.1412	-0.0268	0.1033
		0.3723	0.0473	0.1305	0.0418		-0.1394	-0.0476	-0.1337

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_2 diallel set at two locations.

TABLE 30. Number of seeds per spike

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	1.1545	-0.7005	0.1160	0.5999	3.1883	9.3728	-1.9670
			0.2870	-0.0244	1.3941	0.6768	2.2384	4.0955	-2.2876
Chinook		0.7028	-	0.0982	-0.0284	2.0048	-1.5763	1.6979	-1.5227
		0.1278		0.0492	-0.1192	0.7419	-1.1155	0.3293	-2.2601
Khush-hal		0.1287	-1.4832	-	0.2428	-1.4129	-1.7061	2.1238	-1.8002
		-1.2997	0.0360		-1.8748	-0.5793	0.2738	-0.8401	-2.2866
Ciano		0.7217	0.9697	-0.1442	-	1.3696	-2.1989	4.0483	-1.9426
		0.7168	-1.2167	0.3277		0.7678	-2.4832	5.2511	-0.4635
Inia		1.7125	-0.0612	1.0087	0.5783	-	2.2930	4.4710	0.7809
		0.9752	0.4083	-0.7652	1.0390		1.0865	-0.2653	-1.6431

Reciprocal effects

TABLE 31. Weight of seeds per spike

Marquis		-	-0.0530	0.0072	0.0107	0.1000	0.0283	-0.0017	-0.0064
			0.0068	-0.0384	0.0898	0.1372	-0.0274	-0.0018	-0.0063
Chinook		0.0022	-	-0.0560	0.0218	0.0196	-0.1592	0.0228	-0.0054
		0.0172		-0.0018	-0.0060	-0.0131	-0.1023	0.0079	-0.0063
Khush-hal		-0.0283	-0.0740	-	0.0447	-0.0299	-0.0475	-0.0003	-0.0053
		-0.0558	-0.0208		-0.0383	0.0114	0.0665	0.0019	-0.0058
Ciano		0.1072	0.0355	-0.0413	-	-0.0030	-0.0079	-0.0025	-0.0055
		0.0700	-0.0573	-0.0225		0.0051	-0.0431	-0.0007	-0.0031
Inia		0.0237	0.0072	-0.0377	-0.0052	-	0.1863	0.0322	-0.0026
		0.0885	-0.0143	-0.0503	0.0277		0.1063	0.0088	0.0001

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

With respect to final heading (Table 25) and heading-span (Table 26), although there are some differences in relative positions of the parents and hybrids concerned, the general conclusions are the same as for onset-of-heading.

Cross (MxCH) at Ellerslie and (MxK) at Parkland ranked highest for plant height while (MxI) at both locations was the lowest (Table 27). Cross (MxCH) had both parents with highest GCA's at both locations while cross (MxK) with highest SCA at Parkland had one parent (Khush-hal) with a comparatively low GCA. Similarly (MxI) with lowest SCA at both locations had Marquis parent with highest GCA at both locations. In all cases the variances for GCA were greater than those for SCA. Crosses (CxCH), (IxM) and (IxCH) at both locations and (KxM) at Ellerslie showed significant reciprocal effects, which may be ascribed to the female parents because of the positive sign appended to each effect.

For number of tillers per plant (Table 28), crosses (KxC) at Ellerslie and (CHxK) at Parkland scored highest in SCA and (CHxC) at Ellerlie and (MxCH) at Parkland scored lowest. It is again noteworthy that one parent of the hybrids with high SCA (Ciano) had the second lowest GCA at both locations, while one parent of those scoring lowest in SCA (Chinook) had the highest GCA at both locations. The variances for GCA were, in general, greater than those for SCA and the reciprocal effects were non-significant.

The general interpretations for the remaining components of yield, viz., number of spikelets per spike (Table 29), number of seeds per spike (Table 30), weight of seeds per spike (Table 31) and 1000-kernel

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F_2 diallel set at two locations.

TABLE 32. 1000-kernel weight

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	-0.0159	0.2364	-0.1336	1.4490	-2.0321	3.4447	-1.7115
			-0.2108	-0.8323	1.4480	2.2354	-2.2536	4.5162	-1.4056
Chinook		-0.5203	-	-1.4490	0.4314	-1.1334	-2.2150	4.3318	-1.7114
	Reciprocal effects	0.2470		0.1446	-0.2289	-0.7060	-1.3656	1.3026	-1.3909
Khush-hal		-1.2750	-0.4182	-	0.9701	0.9718	0.4223	-0.5063	-0.9926
		-0.2907	-0.5318		0.3904	0.9605	1.2445	0.9866	-1.1678
Ciano		1.6177	0.0647	-1.0387	-	-1.8572	1.7856	2.5039	-1.3299
		0.2192	-0.3352	-0.0517		0.3992	1.2144	0.9125	-0.6385
Inia		-0.7592	0.1358	-0.8753	-0.6647	-	2.0392	3.4739	0.3453
		1.0892	-0.5033	-0.2993	-0.3512		1.1603	0.7840	0.7868

TABLE 33. Yield per plant

Marquis		-	0.5420	-0.8646	1.1590	-0.1661	0.0508	-0.3966	-0.9980
			-0.8039	0.7455	0.0267	0.7448	-0.5307	-0.1445	-1.0655
Chinook		-0.4107	-	0.1689	-1.0782	0.1929	-1.4712	1.7653	-0.9001
	Reciprocal effects	0.6045		1.3541	-0.7700	0.3538	0.1256	-0.4104	-0.8501
Khush-hal		2.1502*	0.5530	-	1.7764	-0.4546	-0.7275	0.1300	-0.7394
		-1.5562	-0.0635		0.0255	-1.2061	0.6319	-0.0270	-0.2690
Ciano		-0.9003	-0.1892	-0.4672	-	0.0659	0.6961	0.0854	0.8891
		1.3395	-0.1583	-0.2452		0.1652	-0.5374	-0.1373	-0.8674
Inia		1.0152	1.1928	0.6962	-0.4528	-	1.4518	1.7084	-0.9061
		0.5628	-0.4918	-0.3988	-0.1468		0.3109	-0.3296	-0.3448

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

weight (Table 32) and the conclusions derived therefrom with respect to SCA's do not differ from number of tillers per plant. Only the relative positions and respective ranking orders of the parents and hybrids are changed.

For yield per plant (Table 33), crosses (KxC) at Ellerslie and (CHxK) at Parkland, respectively scored highest in SCA while (CHxC) at Ellerslie and (KxI) at Parkland ranked lowest. One parent of (KxI), Inia, scored highest for GCA at both locations while one parent of (CHxC), Chinook, scored lowest at Ellerslie and other parent, Ciano, scored second highest at Ellerslie. (KxC) had one parent (Khush-hal) with the second lowest GCA at Ellerslie. The variances for GCA were greater than those for SCA except for Marquis and Ciano at both locations, and Chinook, Khush-hal and Inia at Parkland. The reciprocal effects were non-significant except for (KxM) at Ellerslie which may be ascribed to Khush-hal because of the positive sign appended to the effect.

The following conclusions may be drawn from the analysis of general and specific combining ability for all the characters considered: (1) In all cases, since hybrids with high SCA's were associated with the parents with low GCA's, the high GCA's of the parental lines may not be taken as criteria to predict high SCA's of their hybrids. (2) In most cases, the variances for GCA's were greater than those for SCA's. The analysis of variance for general and specific combining ability (Table 34) also supports this conclusion. In all cases, the mean squares for GCA in Table 34 are significant except for heading-span and yield per plant at Parkland. This implies that GCA which is largely due to

TABLE 34

Analysis of variance of general and specific combining ability and reciprocal effects from F_2 diallel set for ten characters at two locations.

Character	M.S. for GCA	M.S. for SCA	M.S. for reciprocal effects	Error M.S.
D.F.	4	10	10	48
Onset-of-heading	22.7031**	2.1187**	0.4000	0.2390
	39.0469**	4.0062**	0.2431	0.5096
Final heading	31.3750**	2.3062**	0.5625*	0.2126
	46.0000**	5.6812**	0.3375	0.7635
Heading-span	1.3652*	0.5275*	0.2319	0.2507
	1.5268	1.9586*	0.4347	0.9094
Plant height	1169.9375**	17.7062**	47.0742**	4.4982
	1415.1094**	25.2250**	27.7873	39.3587
Number of tillers per plant	1.9502*	0.8808	0.5834	0.6970
	9.3584**	1.0986	0.4896	1.2179
Number of spikelets per spike	3.0322**	0.2066	0.2304	0.1753
	3.2627**	0.2785	0.0921	0.9593
Number of seeds per spike	64.1406**	3.4828	1.6961	2.9497
	34.2031*	2.9781	1.3182	10.7170
Weight of seeds per spike	0.1579**	0.0063	0.0046	0.0096
	0.0720*	0.0126	0.0048	0.0163
1000-kernel weight	41.4063**	2.6574	1.5148	2.5674
	28.2812**	3.3535	0.4488	6.8000
Yield per plant	13.2227**	1.8699	1.8725	1.4968
	2.7109	1.3242	1.0820	2.2172

First reading under each column refers to Ellerslie and the second to Parkland.
* Significant at 5% level
** Significant at 1% level

TABLE 35

Mean squares from the analysis of variance of 5 x 5 F_2 diallel set for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Final heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
a	4	68.0938**	73.1250	4.0957	3510.5000**	5.8467	9.0908**	192.3750**	0.4738**	124.1875**	39.6543**
		117.0937**	138.1719**	4.5820	4245.5000**	28.0713**	0.7852*	190.9219*	0.2159**	84.8125**	8.1191
b	10	6.3812**	61.2437	1.5824	53.0000**	2.6473	0.6227	10.5312	0.0188	7.9812	5.6172
		12.0687**	17.0125**	5.8754	75.7000*	3.2988	0.8395	68.5313	0.0377	10.0750	3.9770
b_1	1	36.7496	79.5675	0.0208	6.4820	1.0448	0.2168	3.8458	0.0116	0.0029	5.3993
		51.6675	82.6875	3.7408	10.0833	10.2491	1.0195	40.0176	0.0698	23.5447	1.3118
b_2	4	4.1406	44.9219	0.9528	59.7031	1.0060	0.0586	17.0752	0.0249	9.5039	4.0752
		4.2607*	5.1094	7.6094	93.1250*	3.9525	0.9189	75.6230	0.0582	9.9443	1.6973
b_3	5	2.1000**	70.6500*	2.3992	56.9000**	4.2852*	1.1625	6.6250	0.0156	8.3625	6.8337*
		10.3750**	13.4250**	4.9156	74.6125*	1.3898	0.7453	68.5625	0.0149	7.5000	6.3586**
c	4	2.2541	71.7542	0.5375	239.1516**	2.8807	0.4980	8.5938	0.0072	2.2230	6.1870
		1.1625	0.5542	2.0292	141.6374**	1.7982	0.1374	93.4017	0.0091	1.3426	1.2746
d	6	0.4972	56.6431	0.8014	75.9351**	0.9963	0.8198*	2.7512	0.0180	6.0919	5.2380
		0.4403	1.3181	0.8208	44.5118*	1.2493	0.3691	83.4116	0.0178	1.3488	4.5601
Blocks x *a*	8	0.6094	35.5859	1.2484	22.0469	1.7603	0.7969	8.4609	0.0289	14.6484	3.1318
		2.6172	2.0547	5.3865	59.4609	3.1372	1.4517	30.6875	0.0298	7.3843	12.6904
Blocks x *b*	20	0.8375	42.0594	0.8220	14.4500	2.9328	0.6846	12.5031	0.0395	7.5344	4.9916
		1.2875	3.4312	3.5931	24.2156	2.8902	0.5980	67.5125	0.0373	9.5287	3.4434
Blocks x b_1	3	4.4151	17.8850	1.7017	30.5184	3.0592	1.7195	63.1927	0.0729	8.1275	5.6767
		7.9850	19.1850	3.0817	181.8318	30.4553	0.1034	36.0421	0.1419	51.5334	10.3759
Blocks x b_2	8	1.2827	23.4004	1.2711	22.0747	5.5184	0.8450	15.7554	0.0651	11.1401	9.3918
		1.0347	4.0889	5.8386	18.0625	2.8100	0.9053	53.9883	0.0589	10.5664	6.4728
Blocks x b_3	10	0.1875	63.5938	0.4566	8.3312	1.1415	0.5141	6.0937	0.0196	5.3578	1.8984
		0.9437	1.6625	2.2068	16.0437	0.4828	0.4585	88.4437	0.0133	5.4691	0.6773
Blocks x *c*	8	0.9041	71.3666	0.4500	9.2411	1.2472	0.2572	4.8894	0.0130	3.9115	3.0324
		0.7812	0.8979	1.4104	3.1023	1.5910	0.4212	60.4627	0.0084	1.1626	2.6685
Blocks x *d*	12	0.4597	57.7347	0.5056	9.1118	1.4759	0.2664	5.7155	0.0207	5.9257	5.5405
		1.6944	1.5056	0.4000	11.1003	1.2713	0.7791	94.8401	0.0262	3.7547	3.2056
Error	48	0.7161	49.7838	0.7520	13.5133	2.0922	0.5275	8.8636	0.0286	7.7141	4.4923
		1.5265	2.2982	2.7299	23.2919	3.3101	0.7561	67.0319	0.0285	6.3335	4.7959

*Significant at 5% level
**Significant at 1% level
First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of (a-1)(r-1). Each component has been tested against its own block interaction.

TABLE 36

Analysis of variance of W_p-V_p from F_2 diallel set for ten characters at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.
Onset-of-heading	7.3043	0.2675	0.4078
	8.3904	2.4463	0.8019
Final heading	2.3424	0.7644	0.2218
	35.5057	5.2120	3.7671
Heading-span	0.0046	0.1472	0.2028
	0.1741	4.4720	2.0416
Plant height	10448.0312	150.1719	157.5547
	4912.7812	427.7812**	38.5703
Number of tillers per plant	1.2452	2.4152*	0.5435
	0.8319	0.5920	2.3435
Number of spikelets per spike	0.9966	0.0884	0.0807
	0.0373	0.1622	0.0598
Number of seeds per spike	616.7512	26.2899	19.7865
	188.8423	15.5951	6.5623
Weight of seeds per spike	0.0089	0.0002	0.0003
	0.0025	0.0004	0.0003
1000-kernel weight	313.4819	7.3413	1.9490
	2.8203	11.5522	18.5395
Yield per plant	61.8167	9.5905	3.0673
	12.4054	2.6444	2.7121

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
**Significant at 1% level

TABLE 37

Estimates of second degree statistics parameters for ten characters from F_2 diallel set at two locations.

Character	V_{OLD}	W_{OLDR}	V_{OLR}	V_{ILD}	$(W_{LL}-W_{LO})^2$
Onset-of-heading	15.0000	5.8158	3.2734	3.3381	1.9600
	15.7002	7.6168	30.9072	5.9148	3.7759
Final heading	10.9688	7.2016	3.1475	4.3006	1.5891
	27.1914	11.1402	4.6084	7.4500	4.4100
Heading-span	0.5889	0.2362	0.1367	0.4003	0.0011
	3.6100	0.6751	0.1528	1.1320	0.1995
Plant height	486.7784	235.7205	117.0059	125.8615	0.3456
	518.4434	226.4807	141.5420	154.1387	0.5377
Number of tillers per plant	1.4343	0.5030	0.1948	0.6359	0.0557
	5.4749	2.1069	0.9358	1.4856	0.5465
Number of spikelets per spike	1.2283	0.6072	0.3030	0.4072	0.0115
	0.5749	0.4241	0.3264	0.4063	0.0543
Number of seeds per spike	28.9930	12.8064	6.4111	8.1627	0.2050
	12.2275	5.6126	3.4160	4.9113	0.2783
Weight of seeds per spike	0.0384	0.0241	0.0158	0.0189	0.0006
	0.0360	0.0133	0.0072	0.0135	0.0037
1000-kernel weight	16.7744	7.8586	4.1396	5.4666	0.6001
	13.1670	5.6221	2.8271	4.5019	1.2557
Yield per plant	5.4558	2.4823	1.3221	2.2580	0.4412
	0.8875	0.4078	0.2711	0.9338	0.0646

First reading under each column refers to Ellerslie and the second to Parkland.

additive gene effects, is relatively more important than SCA, which is due to non-additive gene effects, as far as selection on the basis of these characters is concerned. (3) The significance of SCA variances implies that hybrids yield much less than would be expected on the basis of the GCA's of their parents. This suggests that character instability of a hybrid is largely due to high SCA variances associated with its parents.

Diallel cross analysis

The results of the analysis of variance performed after Hayman (1954a) on the F_2 diallel table are given in Table 35. The presence of additive gene effects is shown by significant a's for onset-of-heading, plant height, number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight at both locations; also for yield per plant at Ellerslie and final heading and number of tillers per plant at Parkland. Significant additive gene effects for these characters suggest substantial differences among the parental lines used. Significant b's for onset-of-heading, final heading and plant height shows that dominance is present while significant b_2's indicate some asymmetry of loci exhibiting dominance for these characters, suggesting that some parents contain more dominant alleles than others. Significant b_3's for onset-of-heading, final heading, plant height and yield per plant at both locations, and for number of tillers per plant at Ellerlie, imply that specific combining ability for these characters is comparatively more important than general combining ability when a pedigree selection procedure is followed in a breeding programme (Mather and Jinks, 1971).

TABLE 38

Estimates of genetic components of variation and their standard errors from F_2 diallel set for ten characters at two locations.

Character	D	F	H_1	H_2	h^2	E
Onset-of-heading	14.6708 ± 0.2067**	6.4497 ± 0.5162**	4.4673 ± 0.5581**	3.7803 ± 0.5062**	7.6875 ± 0.3418**	0.2391 ± 0.0844**
	15.1911 ± 0.6740**	0.3223 ± 1.6836	7.5679 ± 1.8202**	7.0114 ± 1.6509**	10.6973 ± 1.1146**	0.5091 ± 0.2752
Final heading	16.7506 ± 0.3740**	4.8680 ± 0.9356**	4.8009 ± 1.0115**	4.1802 ± 0.9175**	6.2127 ± 0.6194**	0.2161 ± 0.1529
	28.3875 ± 0.5310**	8.8251 ± 1.3263**	10.4043 ± 1.4339**	9.8386 ± 1.3006**	17.1511 ± 0.8781**	0.7639 ± 0.2166**
Heading-span	0.3383 ± 0.1606*	-0.0677 ± 0.4012	0.5938 ± 0.4337	0.5534 ± 0.3934	-0.1560 ± 0.2656	0.2407 ± 0.0656**
	2.7012 ± 0.7537**	3.4300 ± 1.8827	3.0730 ± 1.9014	2.0971 ± 1.7971	0.2157 ± 1.2133	0.9100 ± 0.2995**
Plant height	482.2761 ± 5.3403**	25.2691 ± 13.3401	35.6431 ± 14.4221**	26.4261 ± 13.0810*	-1.4902 ± 8.8316	4.4983 ± 2.1802*
	510.7024 ± 11.4837**	-38.3252 ± 28.6862	48.9489 ± 31.0130	34.9049 ± 28.1292	-2.8030 ± 18.9913	7.7409 ± 4.6882
Number of tillers per plant	0.7373 ± 0.1694**	0.0199 ± 0.4232	0.1536 ± 0.4575	0.3705 ± 0.4150	-0.2232 ± 0.2802	0.6970 ± 0.0692**
	4.7055 ± 0.1993**	1.5989 ± 0.4978**	0.9894 ± 0.5382	0.6605 ± 0.4881	1.6941 ± 0.3296**	0.7694 ± 0.0814**
Number of spikelets per spike	1.0529 ± 0.0515**	-0.1827 ± 0.1287	-0.0278 ± 0.1391	0.0658 ± 0.1262	-0.0660 ± 0.0852	0.1753 ± 0.0210**
	0.3233 ± 0.1134**	-0.8483 ± 0.2834**	0.0896 ± 0.3064	0.0562 ± 0.2779	0.0565 ± 0.1876	0.2516 ± 0.0463**
Number of seeds per spike	26.0475 ± 1.1122**	3.2297 ± 2.7783	2.7517 ± 3.0037	1.1052 ± 2.7244	-1.0681 ± 1.8394	2.9505 ± 0.4541**
	8.7961 ± 1.0111**	-2.1931 ± 2.5257	0.4207 ± 2.7306	-0.8894 ± 2.4767	-1.0827 ± 1.6721	0.0095 ± 0.0021**
Weight of seeds per spike	0.0288 ± 0.0019**	-0.0313 ± 0.0047**	-0.0073 ± 0.0050	-0.0065 ± 0.0046	-0.0036 ± 0.0031	0.0095 ± 0.0008**
	0.0266 ± 0.0052**	0.0075 ± 0.0130	0.0121 ± 0.0140	0.0062 ± 0.0127	0.0088 ± 0.0086	0.0095 ± 0.0021**
1000-kernel weight	14.2071 ± 0.8036**	-0.9663 ± 2.0075	0.5315 ± 2.1703	0.1733 ± 1.9685	1.6424 ± 1.3290	2.5673 ± 0.3281**
	11.0585 ± 1.3289**	1.3155 ± 3.3195	3.2122 ± 3.5888	2.4900 ± 3.2551	3.6732 ± 2.1976	2.1085 ± 0.5425**
Yield per plant	3.9588 ± 0.7287**	-0.8142 ± 1.8203	0.6660 ± 1.9679	0.7492 ± 1.7849	0.1937 ± 1.2051	1.4970 ± 0.2975**
	-0.7108 ± 0.3318*	-1.7740 ± 0.8287*	-1.1636 ± 0.8960	-0.5453 ± 0.8126	-0.7644 ± 0.5487	1.5982 ± 0.1354**

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
**Significant at 1% level

TABLE 39

Proportional estimates of genetic parameters for ten characters from F_2 diallel set at two locations.

Character	$[H_1/D]^{1/2}$	$[H_2/4H_1]$	$\left[\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}\right]$	$r_{(Y_r/W_r+V_r)}$	$\left\|\frac{h^2}{H_2}\right\|$	[Heritability]
Onset-of-heading	0.5501*	0.2116*	2.3175*	0.9658	2.0336*	1.0751
	0.7058*	0.2316*	1.0305†	0.8792	1.5257*	0.6206
Final heading	0.5354*	0.2177*	1.7451*	0.9906	1.4862*	0.9545
	0.6279*	0.2364*	1.7279*	0.9550	1.7432*	0.8596
Heading-span	1.3249	0.2330	0.8596	0.9362	-0.2818	0.1689
	1.0666	0.1706	3.9415	0.2426	0.1028	0.4513
Plant height	0.2719*	0.1854*	1.2131†	0.7522	-0.0566	0.9443
	0.3096	0.1783	0.7838	0.0827	-0.0803	0.8120
Number of tillers per plant	0.4565	0.6029	1.0610	-0.1501	-0.6023	0.2015
	0.4585	0.1669	2.1772	0.9489	2.5648	0.6559
Number of spikelets per spike	0.1626	-0.5913	0.3040	0.8604	-1.0027	0.5515
	0.5264	0.1569	-0.4273	-0.1745	1.0043	0.1425
Number of seeds per spike	0.3250	0.1004	1.4714	0.0765	-0.9664	0.6969
	0.2187	-0.5285	0.2739	-0.1187	1.2174	0.7683
Weight of seeds per spike	0.5034	0.2241	-0.0379	-0.2629	0.5555	0.3171
	0.6752	0.1272	1.5290	-0.3126	1.4330	0.3843
1000-kernel weight	0.1934	0.0815	0.7009	-0.5825	-9.4800	0.5469
	0.5390	0.1938	1.2481	-0.8244	1.4752	0.5170
Yield per plant	0.4102	0.2812	0.5991	0.1919	0.2585	0.3464
	1.2795	0.1172	0.0125	-0.4069	1.4016	-0.1129

First reading under each column refers to Ellerslie and second to Parkland.
*Genetic components of variation for the characters significantly different from zero at $P \leq 0.05$
†Components D and H_1 significant, F non-significant ($P > 0.05$).

In regard to the testing of the assumptions underlying the analysis, significant c's for plant height at each of the two locations indicate that there are reciprocal differences for this character. The results of a test of other assumptions, by the analysis of variance of W_r-V_r differences are given in Table 36. Except for plant height at Parkland and number of tillers per plant at Ellerslie, the W_r-V_r differences were homogeneous and therefore these other assumptions were generally not invalidated by the data. Two exceptions (for plant height and number of tillers per plant) will be considered later.

Estimates of second degree statistics and components of genetic variation derived from the analysis of F_2 diallel table after replacement of off-the-diagonal cells with their corresponding common means, are given in Tables 37 and 38. In Table 38, component significances are tested with 25 D.F. (35 statistics provided by Table 37, with 10 constants fitted to them). Proportional values of the genetic parameters calculated from Table 38 are given in Table 39, which shows the over-all genetic situation with regard to the inheritance of each character. The results of Tables 38 and 39 together with W_r,V_r graphs and standardized deviation graphs of Y_r and (W_r+V_r) are discussed under each character.

All components of variation for onset-of-heading (Table 38) except F and E at Parkland were significant. The mean degree of dominance (0.55 at Ellerslie and 0.75 at Parkland) indicates that the character is partially dominant at both locations. This is also shown by the regression line in the W_r,V_r graph (Figure 21) which intersects the limiting parabola

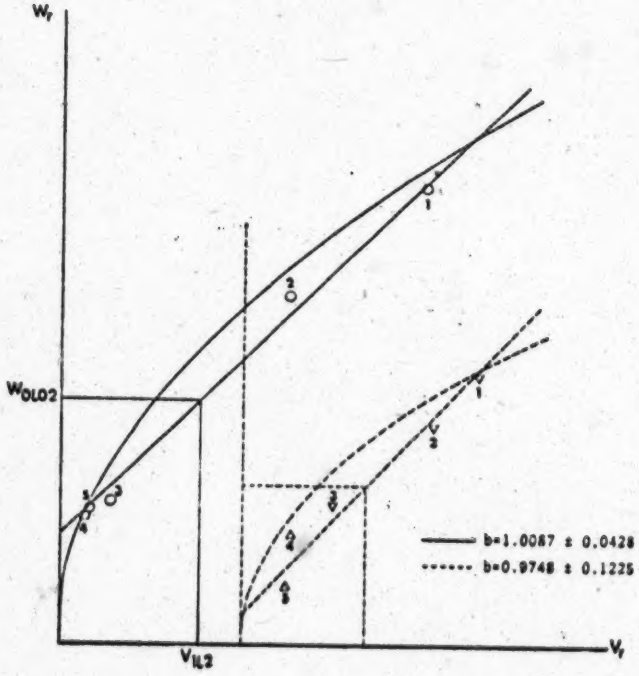

Figure 21. W_r, V_r graph for onset-of-heading from F_2 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

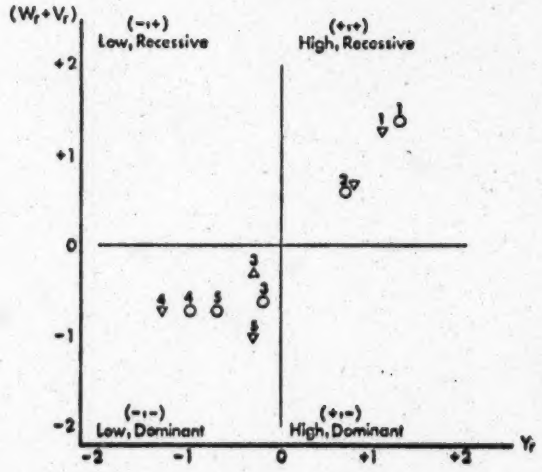

Figure 22. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from F_2 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

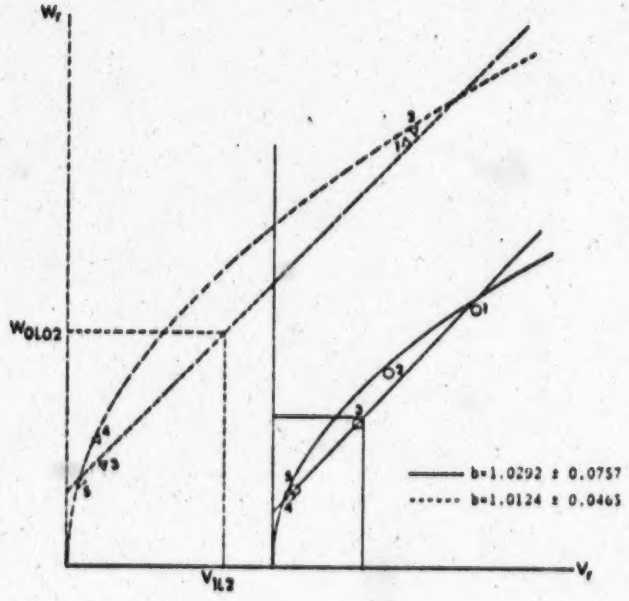

Figure 23. W_r, V_r graph for final heading from F_2 diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

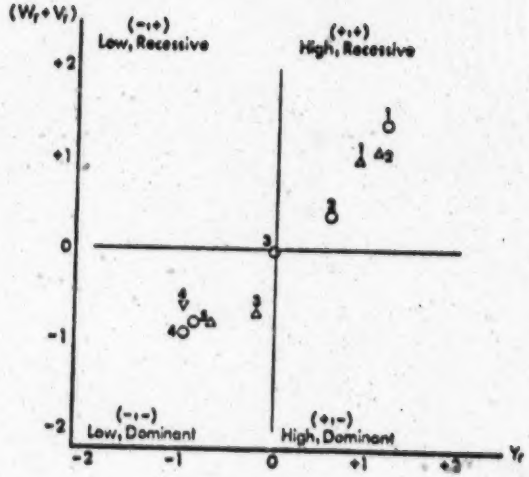

Figure 24. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from F_2 diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

above the origin. The proportion of positive to negative alleles in the parents at loci exhibiting dominance is approximately 0.25, indicating equal proportions at both locations. The proportion of dominant to recessive genes in the parents is 2.3 and 1.03 for Ellerslie and Parkland, suggesting a preponderance of dominant genes in the parents. Figure 21 shows that Marquis is the highly recessive parent at both locations, as it lies farthest from the point of origin of the regression line. Ciano at Ellerslie and Inia at Parkland rank as the two most dominant parents because of their nearness to the point of origin of the regression line. The coefficient of correlation between parental order of dominance and parental measurements is 0.96 at Ellerslie and 0.87 at Parkland suggesting that most of the negative genes (for early maturing) are dominant. The distribution of parents with respect to order of dominance is shown in standardized deviation graph of Figure 22. Marquis and Chinook at both locations fall into the (+,+) quadrant indicating that they contain mostly recessive genes responsible for lateness while Khush-hal, Ciano and Inia fall into the (-,-) quadrant and are therefore early heading dominant parents. The number of groups of genes controlling onset-of-heading has been estimated as 2.03 for Ellerslie and 1.52 for Parkland indicating that at least two groups of genes exhibiting dominance control the onset-of-heading. The heritability estimates of 107.51% and 62.06% show that the character is highly heritable but with low stability under different environments.

The results of the analysis for final heading (Tables 38, 39; Figures 23, 24) and heading-span (Tables 38, 39; Figures 25, 26) are subject

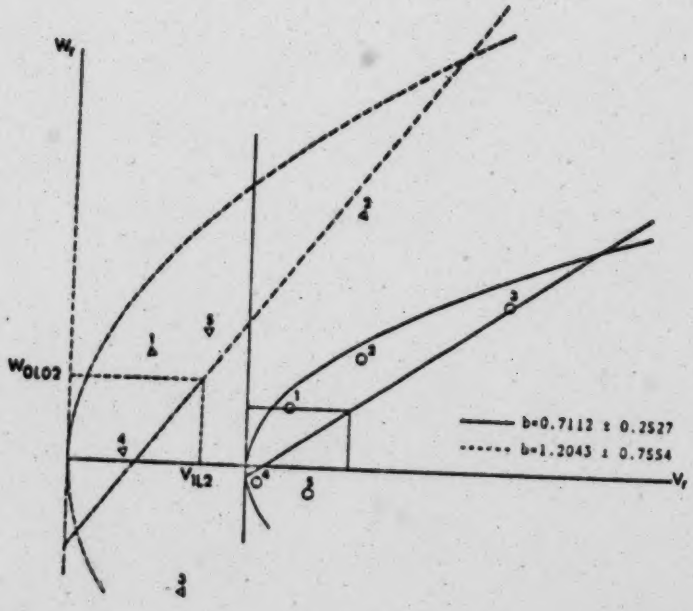

Figure 25. W_r, V_r graph for heading-span from F_2 diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

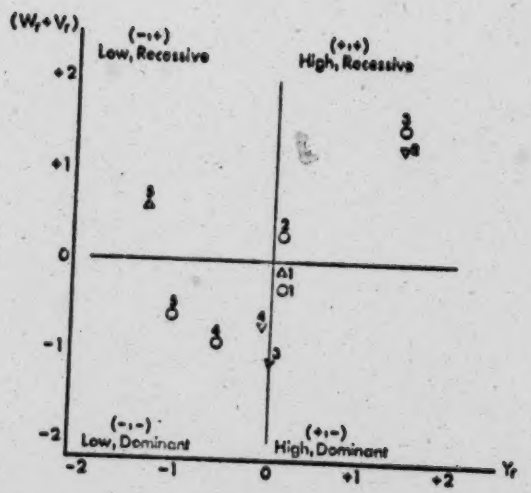

Figure 26. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from F_2 diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $W_r + V_r]$ intercepts at Parkland

to the same kind of interpretations as for onset-of-heading.

For plant height, the components of variation, D, H_1, H_2 and E were significant for Ellerslie but none except D were significant at Parkland. Heterogeneity of W_r-V_r values (Table 36) implies either non-allelic interaction, multiple allelism or correlated gene distribution. In the case of correlated gene distribution, the W_r,V_r curve is convex upwards and the mean degree of dominance is seriously inflated, giving an impression of apparent over-dominance (Hayman, 1954b) in a situation where, in fact, partial dominance exists. In the case of multiple allelism, the effects are extremely complicated. Models to explain the consequences in terms of W_r, V_r graphs, are pending. It might show spurious dominance (Hayman, 1954b) by scattering the W_r,V_r points and thus causing their mean (V_{1L2},W_{0L02}) to lie inside, and not on the limiting parabola. Non-allelic interaction of the complementary type distorts the (W_r,V_r) graph, inflates the $(H_1 + D)^{1/2}$ and depresses (h^2/H_2), but has very little effect on the estimator of gene frequency. A duplicate type of interaction depresses (h^2/H_2) by increasing the proportion of dominants, but does not alter $(H_1 + D)^{1/2}$, $H_2/4H_1$ and the W_r,V_r graph.

Considering the various effects of the three above-mentioned conditions, and examining the W_r,V_r graph for plant height at Parkland (Figure 27) we come to the conclusion that there is actually no non-validity of any of the above-mentioned hypotheses. This is because the regression of W_r upon V_r is not significantly different from one, the array W_r,V_r intercepts do not show any convexity upwards or downwards

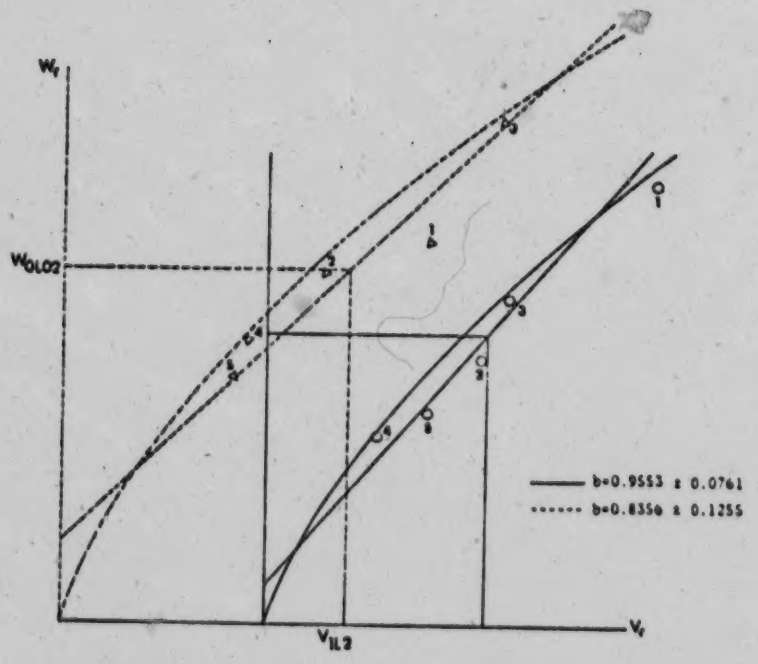

Figure 27. W_r, V_r graph for plant height from F_2 diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

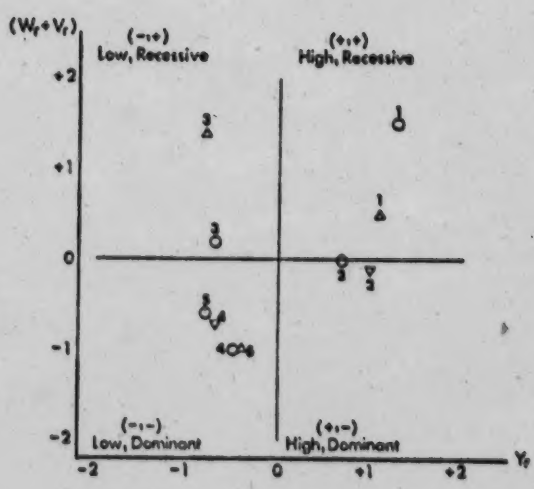

Figure 28. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from F_2 diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $W_r + V_r]$ intercepts at Parkland

and there are no serious effects on the estimates of genetic parameters (Table 39). Our conclusion is supported by the fact that all the estimates of genetic components of variation at Parkland except D are non-significant (Table 38). The only reason we might give for the heterogeneity of W_r-V_r over the arrays is a strong environmental effect.

At Ellerslie, plant height is inherited as a partially dominant trait since the mean degree of dominance is 0.27 (See also Figure 27). The proportion of positive to negative alleles at loci exhibiting dominance is 0.18 indicating asymmetry, while the proportion of dominant to recessive genes in the parents is 1.2 (close to equality). The coefficient of correlation between the parental order of dominance and parental measurements is 0.75 at Ellerslie and 0.08 at Parkland, indicating that the genes contributing towards shortness are mostly dominant. With respect to parental order of dominance (Figure 27 and 28) Marquis rates as the highly recessive parent for tallness at Ellerslie and Khush-hal likewise at Parkland. Ciano ranks as the most dominant parent for shortness at Ellerslie and similarly Inia at Parkland. Examination of Figure 28 reveals that though Marquis and Khush-hal rank as the highly recessive parents, Khush-hal nevertheless contributes towards reduced expression of the character (-,+ quadrant) as compared to Marquis (+,+ quadrant). Ciano and Inia rank as the most dominant parents for shortness because of their position in the (-,-) quadrant. Chinook, contributing towards tallness, has recessive and dominant genes in equal proportions. The character has high heritability (94.43% at Ellerslie and 81.20% at Parkland) and thus seems to be little affected by environmental conditions.

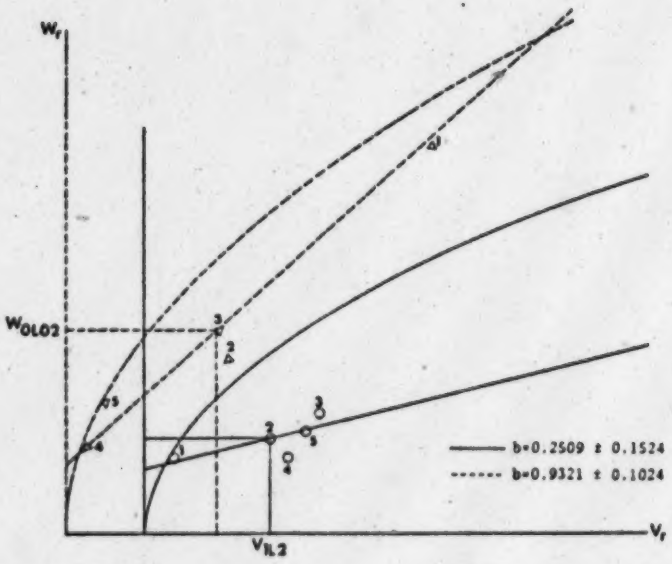

Figure 29. W_r, V_r graph for number of tillers per plant from F_2 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

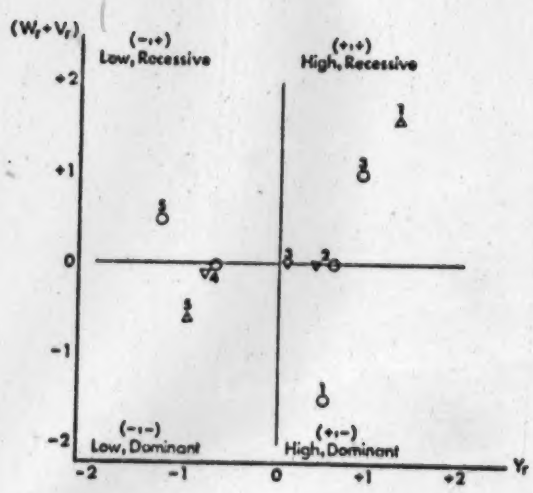

Figure 30. Standard deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from F_2 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

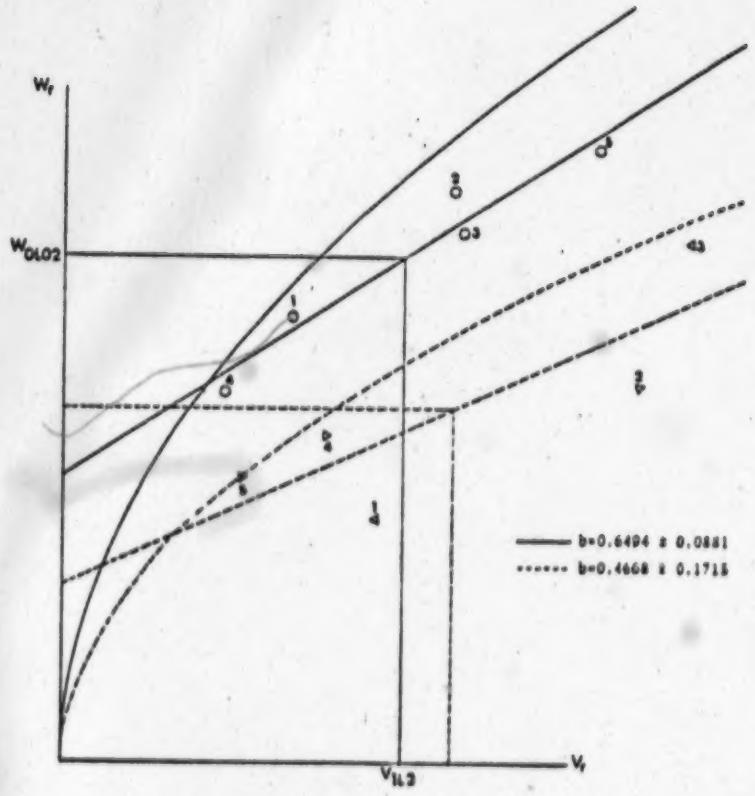

Figure 31. W_r, V_r graph for number of spikelets per spike from F_2 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

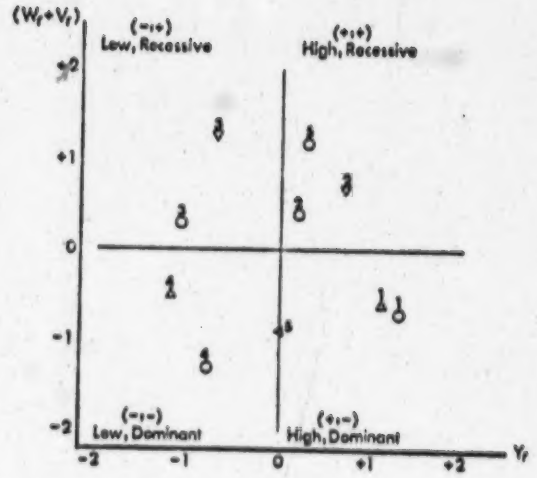

Figure 32. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from F_2 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

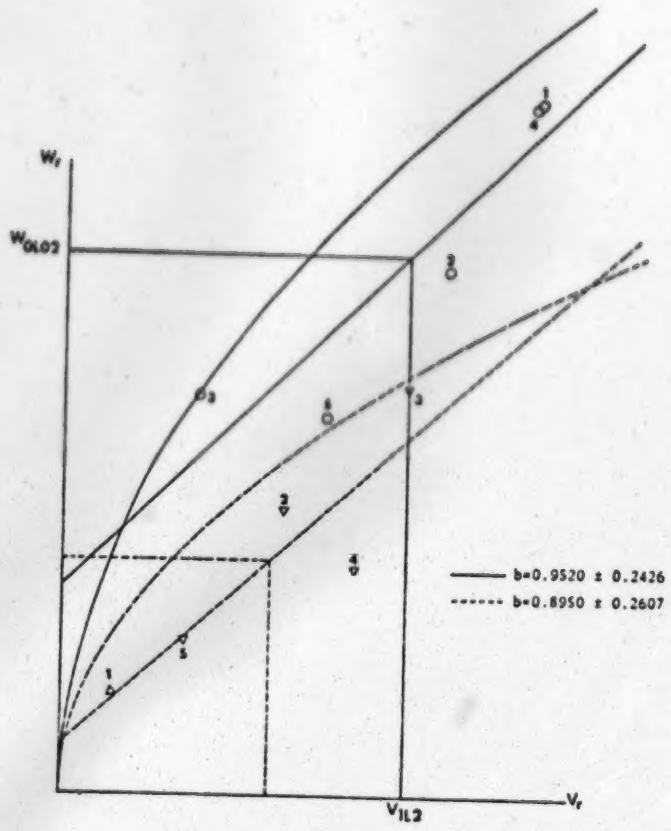

Figure 33. W_r, V_r graph for number of seeds per spike from F_2 diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

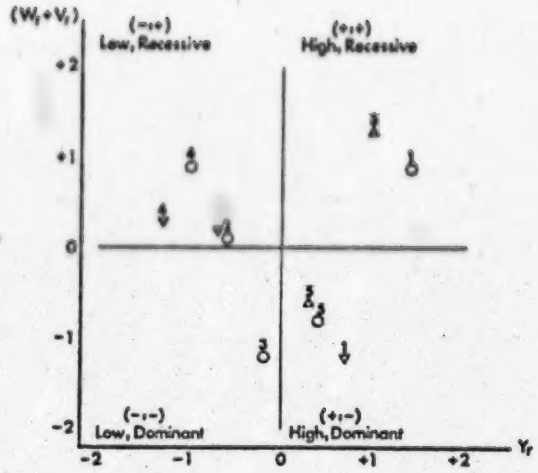

Figure 34. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from F_2 diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

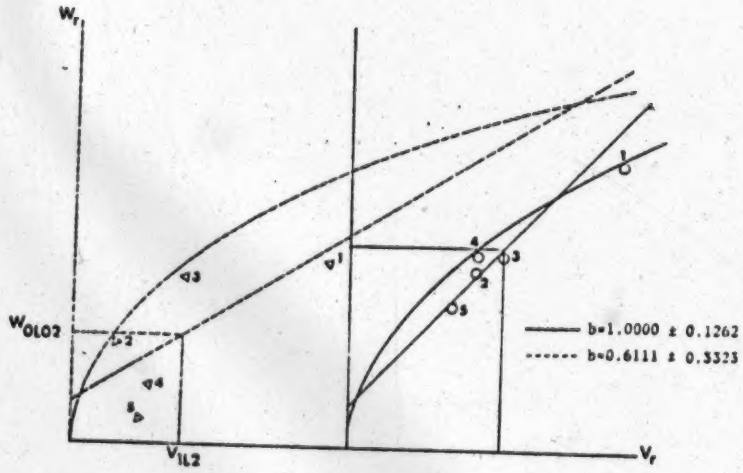

Figure 35. W_r, V_r graph for weight of seeds per spike from F_2 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

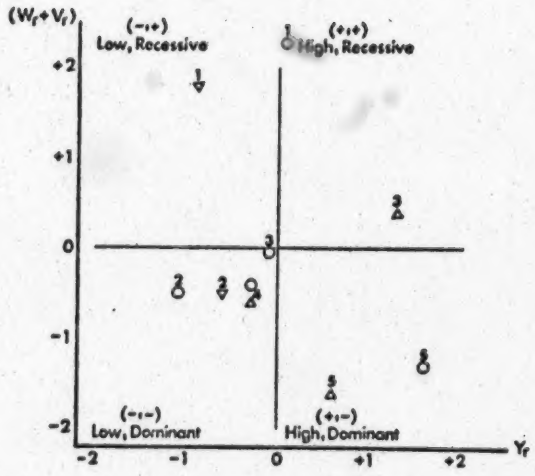

Figure 36. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from F_2 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

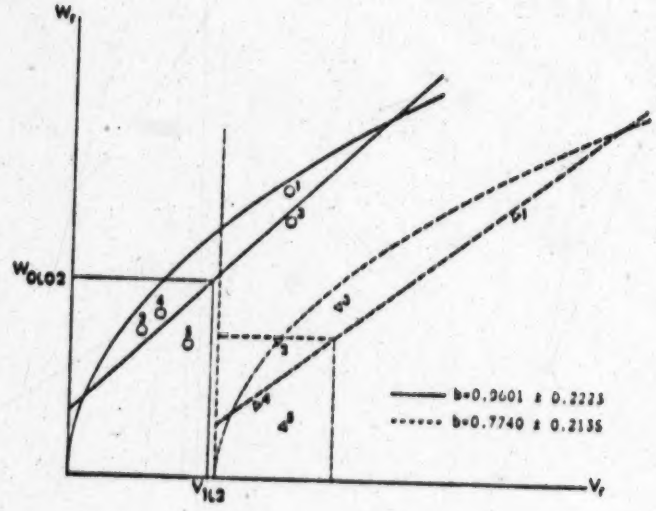

Figure 37. W_r, V_r graph for 1000-kernel weight from F_2 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

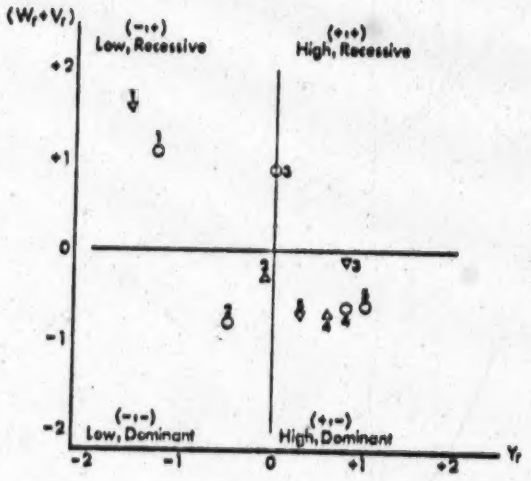

Figure 38. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from F_2 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

Number of tillers per plant showed heterogeneity of $W_r - V_r$ values (Table 36). Examination of the W_r, V_r graph (Figure 29) and a review of the effects of non-allelic gene interaction, multiple allelism and correlated gene distribution upon the analysis, reveals that none of these conditions invalidate the corresponding null hypotheses. Moreover, since at Ellerslie the environmental component of variation is highly significant and all other components of genetic variation but D non-significant, the environmental variation is the most probable reason for heterogeneity of $W_r - V_r$ values. Since the ratios (Table 39) expressing the mean degree of dominance, the proportion of alleles with positive and negative effects at loci exhibiting dominance, the proportion of dominant and recessive genes in the parents and the number of groups of genes controlling the character were based on parameters some of which were not significant (Table 38) their interpretation as well as the interpretation of the graphs is of little value.

The general features of the diallel analysis with respect to the interpretation of the results from Tables 38 and 39 for other yield components, viz., number of spikelets per spike (Figures 31, 32), number of seeds per spike (Figures 33, 34), weight of seeds per spike (Figures 35, 36) and 1000-kernel weight (Figures 37, 38) are the same. The conclusions drawn therefrom differ with respect to the relative position of the parents for their ranking order of dominance.

For yield per plant, only D and E components of variation

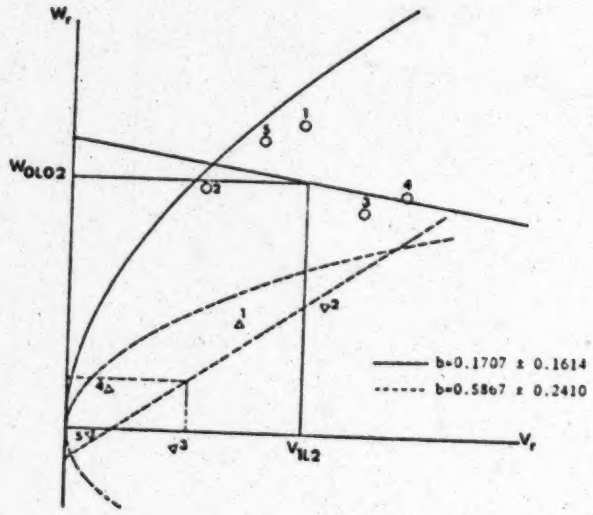

Figure 39. W_r, V_r graph for yield per plant from F_2 diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

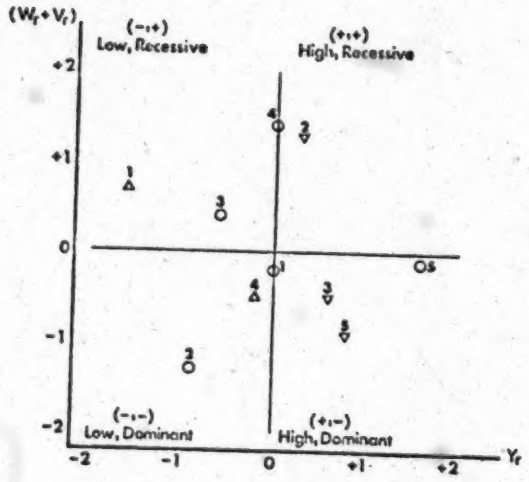

Figure 40. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from F_2 diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

were significant at Ellerslie while D, F and E at Parkland. Because of non-significance of other components of variation, the interpretation of estimates of genetic parameters given in Table 39 would be meaningless.

The W_r, V_r and standardized deviation graphs are interesting in their absurdity. The location effect on yield is sufficiently drastic so that the regression line, though cutting the limiting parabola above its origin (apparent partial dominance) shows a negative slope. The latter (at Ellerslie) implies that for every increase in variance of the rth array, there is a proportional decrease in parent-offspring covariance of that array. The regression line, in this case, cuts the limiting parabola in such a way that the recessive and dominant W_r, V_r array intercepts are difficult to define. However Figure 39 suggests that Ciano may be regarded as the highly recessive and Chinook the most dominant parent. At Parkland, the regression of W_r upon V_r reveals over-dominance. Chinook may be classified as the highly recessive and Inia the most dominant parents. The standardized deviation graph of Figure 40 reveals that, except for Inia, the ranking order for dominance of the parents seems to be altered between locations. Marquis, the recessive parent, with low yielding capacity at Parkland (-,+ quadrant) becomes dominant and comparatively high yielding at Ellerslie (+,- quadrant). Chinook, low yielding and dominant (-,- quadrant) at Ellerslie, becomes recessive and high yielding (+,+ quadrant) at Parkland. A similar

situation exists with Ciano. The coefficient of correlation between the parental order of dominance and parental measurements is 0.19 at Ellerslie and -0.40 at Parkland. A positive but weak correlation at Ellerslie suggests however, that genes responsible for low yielding are mostly dominant, while the comparatively high negative correlation at Parkland indicates that the genes contributing toward increased yielding are mostly dominant. The estimates of heritability seem to be questionable because of the non-significance of relative components of genetic variation.

ANALYSIS OF BACKCROSS DATA

The expected mean of a pair of reciprocal backcrosses is the same as that of F_2 generation of the cross between the two parents provided the differential loci are independent in their action (Jinks, 1956). Therefore, assuming no non-allelic interaction, the expected statistics for the analysis of backcross family means in a diallel set are the same as those for F_2 family means.

In Appendix II there are eighty backcrosses including reciprocals. A complete diallel table for these backcrosses therefore requires an amalgamation of four backcrosses to compute the appropriate means for each of the off-diagonal cells in the diallel matrix. Using the same symbols as in Appendix II, and taking any two parents, the appropriate backcross combinations can be shown to be equivalent to the mean of the corresponding F_2 hybrid. Thus the mean of M(MxCH), (MxCH)M, CH(MxCH) and (MxCH)CH means is equivalent to the (MxCH)F_2 mean, while the mean of M(CHxM), (CHxM)M, CH(CHxM) and (CHxM)CH means is equivalent to the mean of its reciprocal, i.e., (CHxM)F_2 hybrid.

Denoting the parents Marquis, Chinook, Khush-hal, Ciano and Inia as 1, 2, 3, 4 and 5 the following two diallel tables (Tables 40, 41) may be constructed, the one by keeping the parents of rows as recurrent parents and the other by keeping the parents of columns as recurrent parents. The numbers in the brackets in Table 40 and Table 41 denote the F_1 hybrids while those outside the brackets denote the recurrent parents. From these two tables a complete diallel table can be constructed which will correspond statistically to the F_2 diallel table

TABLE 40

Arrangement of backcrosses and reciprocals
in which the parents of rows are kept as recurrent parents.

	1	2	3	4	5
1.	11	11(12) + (12)11	11(13) + (13)11	11(14) + (14)11	11(15) + (15)11
2.	22(21) + (21)22	22	22(23) + (23)22	22(24) + (24)22	22(25) + (25)22
3.	33(31) + (31)33	33(32) + (32)33	33	33(34) + (34)33	33(35) + (35)33
4.	44(41) + (41)44	44(42) + (42)44	44(43) + (43)44	44	44(45) + (45)44
5.	55(51) + (51)55	55(52) + (52)55	55(53) + (53)55	55(54) + (54)55	55

TABLE 41

Arrangement of backcrosses and reciprocals
in which the parents of columns are kept as the recurrent parents.

	1	2	3	4	5
1.	11	22(12) + (12)22	33(13) + (13)33	44(14) + (14)44	55(15) + (15)55
2.	11(21) + (21)11	22	33(23) + (23)33	44(24) + (24)44	55(25) + (25)55
3.	11(31) + (31)11	22(32) + (32)22	33	44(34) + (34)44	55(35) + (35)55
4.	11(41) + (41)11	22(42) + (42)22	33(43) + (43)33	44	55(45) + (45)55
5.	11(51) + (51)11	22(52) + (52)22	33(53) + (53)33	44(54) + (54)44	55

and may therefore be used for the analysis of genetic components of variation as described by Jinks (1956). Thus, for example, if the entry [11(12) + (12)11] above the main diagonal in Table 40 is denoted as x and the corresponding entry [22(12) + (12)22] in Table 41 as y, then the corresponding element of the F_2 diallel table would be $1/2[1/2x + 1/2y] = 1/4(x + y)$. The entries in the remaining cells of the F_2 diallel table are obtained in the same way. Such a table may be called a *synthetic F_2 diallel table*.

Simple coefficients of correlation between the characters on the basis of the *synthetic complete F_2 diallel table* are given in Table 42. Onset-of-heading was positively correlated with final heading plant height, number of tillers per plant, number of spikelets per spike at both locations. It was negatively correlated with weight of seeds per spike at Parkland and 1000-kernel weight at both locations. The correlations with heading-span and yield per plant at both locations and with weight of seeds per spike at Ellerslie were not significant. The correlations of final heading and heading-span with other characters may be interpreted in the same way.

Plant height was positively correlated with number of tillers per plant, number of spikelets per spike at both locations and with number of seeds per spike at Ellerslie. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. No correlations were observed between plant height and yield per plant at either location or with number of seeds per spike at Parkland.

Number of tillers per plant was positively associated with

TABLE 42

Simple correlation coefficients between ten characters from backcross diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.917**	0.214	0.727**	0.332**	0.592**	0.327**	-0.209	-0.607**	-0.118
	0.830**	-0.025	0.714**	0.565**	0.498**	0.291**	-0.289*	-0.627**	-.0111
2. Final heading	-	0.576**	0.818**	0.395**	0.598**	0.292**	-0.305**	-0.679**	-0.179
		0.532**	0.720**	0.671**	0.550**	0.254*	-0.332**	-0.631**	0.096
3. Heading-span		-	0.507**	0.270*	0.218	-0.009	-0.362*	-0.431**	-0.233*
			0.211	0.341**	0.238*	0.027	-0.162	-0.199	0.325**
4. Plant height			-	0.458**	0.710**	0.262*	-0.303**	-0.638**	0.006
				0.538**	0.650**	0.169	-0.470**	-0.708**	-0.106
5. Number of tillers per plant				-	0.305**	-0.041	-0.132	-0.094	0.491**
					0.411**	0.216	-0.289*	-0.531**	0.173
6. Number of spikelets per spike					-	0.604**	0.115	-0.405**	0.149
						0.651**	0.105	-0.460**	0.212
7. Number of seeds per spike						-	0.621**	-0.160	0.116
							0.600**	-0.212	0.236*
8. Weight of seeds per spike							-	0.638**	0.365**
								0.644**	0.444**
9. 1000-kernel weight								-	0.400**
									0.333**
10. Yield per plant									-

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
**Significant at 1% level

number of spikelets per spike at both locations and with yield per plant at Ellerslie. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at Parkland. There was no correlation with number of seeds per spike at either location or with weight of seeds per spike and 1000-kernel weight at Ellerslie and yield per plant at Parkland. The correlations of number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight respectively with other characters may be interpreted in the same way.

Yield per plant was positively correlated with 1000-kernel weight and weight of seeds per spike at both locations, with number of seeds per spike and heading-span at Parkland and with number of tillers per plant at Ellerslie. It was negatively correlated with heading-span at Ellerslie. Correlations with onset-of-heading, final heading and plant height at both locations were not significant.

The results of the factor analysis as the factor loadings of the varimax-rotated five factor matrix are given in Table 43. Approximately 93% of the total variability at both locations was explained by these factors.

The first principal factor was termed *lateness* because of its highest loadings for onset-of-heading and final heading at both locations. This factor negatively contributed towards weight of seeds per spike, 1000-kernel weight and yield per plant at both locations thus confirming the inverse relationship between time of maturity and yield as observed for F_1 and F_2 diallel data. Plant height at Ellerslie and number of tillers per plant contributed proportionately more towards

TABLE 43

Varimax rotated factor matrix for ten characters from backcross diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.986	0.958	0.154	0.023	0.210	-0.005
	0.913	0.721	0.561	0.061	-0.118	-0.248
Final heading	0.982	0.869	0.135	0.026	0.252	0.380
	0.885	0.709	0.532	0.024	-0.009	0.314
Heading-span	0.987	0.182	-0.040	-0.016	0.180	0.959
	0.965	0.171	0.109	-0.038	0.139	0.951
Plant height	0.868	0.621	0.216	0.252	0.501	0.348
	0.915	0.397	0.847	-0.086	-0.163	0.074
Number of tillers per plant	0.883	0.380	-0.139	0.812	0.009	0.243
	0.859	0.883	0.152	0.054	0.027	0.227
Number of spikelets per spike	0.868	0.415	0.659	0.261	0.426	0.105
	0.914	0.173	0.768	0.511	0.068	0.169
Number of seeds per spike	0.924	0.205	0.937	-0.048	-0.024	-0.004
	0.981	0.168	0.211	0.952	0.029	0.012
Weight of seeds per spike	0.984	-0.188	0.702	0.103	-0.642	-0.184
	0.959	-0.274	-0.266	0.732	0.498	-0.169
1000-kernel weight	0.911	-0.473	-0.003	0.232	-0.768	-0.208
	0.892	-0.489	-0.502	-0.012	0.601	-0.199
Yield per plant	0.898	-0.182	0.193	0.880	-0.123	-0.196
	0.904	0.092	0.021	0.167	0.899	0.244
Percent of total Variability explained	92.910	29.523	19.529	16.343	15.894	13.714
	91.870	23.700	23.085	19.029	14.832	12.771

First reading under each column refers to Ellerslie and second to Parkland.

lateness than either the number of spikelets per spike or number of seeds per spike at both locations. *Lateness* explained 29% and 23% of the total variation present in the data for Ellerlie and Parkland respectively.

Number of spikelets per spike, number of seeds per spike and weight of seeds per spike could be grouped into the second factor *yielding ability* at Ellerslie, because of their higher contribution to this factor. At Parkland, this factor was termed *height* since it carried maximum loading for that character. Both the factors explained 19% and 23% variability in the data at respective locations. At Ellerslie, other yield components such as number of tillers per plant and 1000-kernel weight negatively contributed towards *yielding ability* confirming the results of Table 42. At Parkland, onset-of-heading, final heading and number of spikelets per spike had proportionately higher contributions towards *height* while weight of seeds per spike and 1000-kernel weight turned out to be the negative contributors to this factor.

Yield at Ellerslie and *seeds per spike* at Parkland were classified as the third principal factor which explained 16% and 19% of the total variability for respective locations. At Ellerslie, only number of tillers per plant contributed appreciably towards *yield*, otherwise the contributions of number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight were comparatively low. The factor *lateness* also made a very poor contribution towards *yield*. At Parkland, number of spikelets per spike

and weight of seeds per spike were the major contributors towards *seeds per spike*. Plant height and 1000-kernel weight were negatively affected by this factor.

The term *low yield* was selected for the fourth factor at Ellerslie because of the negative loadings for number of seeds per spike, weight of seeds per spike, 1000-kernel weight, yield per plant and the fact that the lowest positive value was found for number of tillers per plant. At Parkland the alternative fourth principal factor was chosen as *high yield* as it carried the highest loading for yield per plant and positive loadings for 1000-kernel weight, weight of seeds per spike, number of seeds per spike, number of spikelets per spike and number of tillers per plant. Onset-of-heading and final heading contributed positively toward *low yield* but negatively toward *high yield*. Plant height revealed an **inverse** relationship with respect to its contribution towards the yield factor at both locations.

The fifth principal factor, classified as *heading period*, explained 13% of the total variation at both locations. It carried maximum loadings for heading-span at both locations. The contribution of yield and its components, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight towards *heading period* was either very low or negative at both locations, indicating an inverse relationship of yield with heading period. The negative contribution of initial heading towards this factor indicates that earlier heading entries take a longer period to complete

TABLE 44

Estimates of general combining ability of five parental lines used in backcross diallelset for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.8350	1.1600	-0.1316	-1.5753	-1.2899
	1.9650	1.4316	-0.0350	-2.4850	-0.8766
Final heading	2.3333	1.4667	-0.0166	-1.8500	-1.9333
	1.8967	2.1800	-0.3450	-2.2034	-1.5283
Heading-span	0.4667	0.4167	0.0917	-0.3083	-0.6667
	-0.0417	0.7750	-0.3500	0.2417	-0.6250
Plant height	14.2345	9.9832	-7.6700	-6.3678	-10.1798
	14.8495	10.2860	-8.0976	-7.7471	-9.2909
Number of tillers per plant	0.3025	0.6791	0.2759	-0.2361	-1.0213
	1.0841	0.4932	0.0704	-0.5536	-1.0940
Number of spikelets per spike	0.8035	0.2629	-0.4382	-0.5110	-0.1172
	0.6312	0.2373	-0.3260	-0.5021	-0.0404
Number of seeds per spike	3.5835	-1.8660	-1.1196	-2.1986	1.6006
	2.0422	-1.2955	0.5107	-2.4295	1.1722
Weight of seeds per spike	-0.0059	-0.1185	-0.0222	-0.0306	0.1771
	-0.0342	-0.0813	0.0577	-0.0309	0.0888
1000-kernel weight	-2.6314	-1.2960	0.3155	1.4580	2.1540
	-2.3445	-0.7879	0.9186	1.4448	0.7690
Yield per plant	0.0570	-0.7077	-0.6801	0.3461	0.9848
	-0.4831	0.2377	-0.0136	-0.0030	0.2419

First reading under each column refers to Ellerslie and second to Parkland.

their maturity. This kind of relationship was found to be in contradiction with the results obtained for F_1 and F_2 diallels.

Combining ability analysis

The general combining ability values of the parental lines used in the backcross diallel are given in Table 44. At both locations, Marquis ranked first in GCA for onset-of-heading and Ciano the lowest, and therefore these parents were regarded as being late and early maturing respectively. Similar interpretations may be given for final heading and heading-span. For plant height, Marquis and Inia at both locations ranked highest and lowest respectively, while for tiller number Chinook at Ellerslie and Marquis at Parkland scored highest. At both locations, Marquis and Ciano possessed the highest and the lowest GCA for number of spikelets per spike and number of seeds per spike respectively. Similar interpretations may be given for other yield components. As far as yield is concerned, at both locations Inia may be regarded as the best combiner, while Chinook at Ellerslie and Marquis at Parkland were the poorest.

The values of specific combining ability for heading data are given in Tables 45, 46 and 47. The results of Table 45 show that the cross (CxI) possessed the highest SCA and (MxI) the lowest at both locations. The best hybrid was associated with the parents with the lowest GCA's at both locations and the worst was from parents with the highest GCA's. The variances for GCA's were larger than those for SCA's. The reciprocal effects were not significant in all cases. Similar

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 45. Onset-of-heading

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.5067	-0.7017	-0.9267	-1.4183	1.8350	3.3042	-0.1577
			-0.1399	0.0351	-0.5150	-1.3733	1.9650	3.7204	-0.3519
Chinook		-0.2917	-	-0.5267	-0.9600	-0.9100	1.1600	1.2825	-0.0721
		-0.5833		0.1100	-1.1483	-0.8816	1.4316	1.9089	-0.3453
Khush-hal		0.0417	-0.4583	-	0.3733	0.3817	-0.1316	-0.0458	0.0989
		-0.1250	-0.6667		-0.2233	0.0850	-0.0350	-0.1395	-0.3474
Ciano		-0.2917	0.3333	0.0417	-	1.1566	-1.5733	2.4122	0.4822
		-0.7083	-0.2083	0.0		0.1600	-2.4850	6.0344	0.1927
Inia		-0.1667	-0.0833	0.0	0.0	-	-1.2899	1.6009	1.2834
		0.0417	0.0	0.1667	-0.0417		-0.8766	0.6277	0.5468

Reciprocal effects

TABLE 46. Final heading

Marquis		-	0.8584	-0.5333	-0.2417	-1.7000	2.3333	5.3936	-0.1267
			-0.3133	-0.7883	-0.8883	-0.8967	1.8967	3.4204	-0.4424
Chinook		-0.2093	-	-0.5416	-0.5000	-0.5000	1.4667	2.1004	0.1189
		-1.0000		-0.2383	-1.1716	-0.9330	2.1800	4.5753	-0.4097
Khush-hal		0.2500	-0.6250	-	-0.4333	0.1917	-0.0166	-0.0504	0.0658
		0.1667	-0.1667		0.6451	0.3450	-0.3450	-0.0579	0.2758
Ciano		-0.2083	0.0833	0.1667	-	0.8584	-1.8500	3.3718	0.0387
		-0.1250	-0.3750	0.6667		0.4117	-2.2034	4.6779	0.4169
Inia		0.3333	0.1667	0.0417	0.1250	-	-1.9333	3.6871	1.1777
		0.2083	0.3750	0.2083	-0.1667		-1.5283	2.1588	0.2101

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 47. Heading-span

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.2500	0.2000	0.6833	-0.2500	0.4667	0.1601	-0.1442
			-0.2000	-0.7833	-0.3333	0.4500	0.0417	-0.1984	-0.5003
Chinook		0.0833	-	-0.1250	0.3583	0.3000	0.4167	0.1159	-0.1234
		-0.4167		-1.3083	0.0167	-0.0750	0.7750	0.4005	-0.4870
Khush-hal	Reciprocal effects	0.2083	-0.1667	-	-0.7750	-0.1667	0.0917	-0.0493	-0.1257
		0.2917	0.5000		0.6417	0.3000	-0.3500	-0.0776	0.2748
Ciano		0.0417	-0.2500	0.1250	-	-0.2676	-0.3083	0.0374	0.2544
		0.5833	-0.1667	0.3333		0.2917	0.2417	-0.1417	-0.3259
Inia		0.5000	0.2500	0.0417	0.1250	-	-0.6667	0.3867	-0.0604
		0.1667	0.3750	0.0417	-0.1250		-0.6250	0.1905	-0.3726

TABLE 48. Plant height

Marquis		-	1.2204	2.4292	0.7733	-5.9562	14.2345	201.2519	-3.4246
			-1.5368	6.4507	3.8329	-4.4574	14.8495	218.5630	-4.8617
Chinook		1.6708	-	0.2537	0.8719	1.8012	9.9832	98.2939	-2.9272
		-0.9280		-0.4441	0.9886	-1.2487	10.2860	103.8567	-4.0744
Khush-hal	Reciprocal effects	2.0138	-1.9303	-	-2.2625	1.5805	-7.6700	57.4592	-1.4352
		1.1430	-2.0403		-1.2273	-0.0541	-8.0976	63.6259	9.0746
Ciano		-2.3949	-2.6567	0.6065	-	0.5592	-6.3678	39.1798	-1.2646
		-1.6303	-1.9159	0.3160		-0.9246	-7.7471	58.0724	0.8631
Inia		4.3464*	2.5614	0.8408	1.1077	-	-10.1798	102.2588	10.4201
		4.2671*	1.7700	-0.0917	0.1983		-9.2909	84.3766	2.5667

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

interpretations for Tables 46 and 47 may be made.

Hybrids (MxK) and (MxI) showed the highest and the lowest SCA for plant height (Table 48) at both locations. The best hybrid at both locations was associated with the parent (Khush-hal) with the second lowest GCA, and the poorest hybrid was associated with one parent (Marquis) having the highest GCA and another (Inia) showing the lowest GCA at both locations. The variances for GCA were greater than those for SCA and the reciprocal effects at both locations were significant only for (IxM). This effect was attributed to the female parent because of the positive sign appended to it.

At both locations, hybrid (CxI) had the highest SCA while (KxI) at Ellerslie and (MxI) at Parkland ranked lowest and produced the lowest number of tillers per plant (Table 49). The best hybrid had a parent with the lowest GCA at both locations, while the poorest ranking hybrids had high GCA parents (Marquis and Khush-hal, respectively). The reciprocal effects were non-significant for all hybrids and GCA variances were usually higher than those for SCA, except for Marquis, Khush-hal and Ciano, all at Ellerslie. The larger SCA variances for the latter parents imply an importance of non-additive gene effects for number of tillers per plant, and reveal instability in the performance of their hybrids.

The results for the other components of yield, such as number of spikelets per spike (Table 50), number of seeds per spike (Table 51) weight of seeds per spike (Table 52) and 1000-kernel weight (Table 53) may be interpreted in a similar way.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 49. Number of tillers per plant

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.0587	0.1659	-0.2478	-0.0077	0.3025	-0.0735	-0.4126
			-0.2333	-0.6416	-0.3376	-0.7573	1.0841	1.0034	-0.4296
Chinook		-0.5267	-	0.2268	0.4683	-0.2315	0.6791	0.2961	-0.4114
		-0.2190		-0.3082	-0.2684	0.0716	0.4932	0.0714	-0.4114
Khush-hal		0.4750	0.0875	-	-0.2497	-0.6937	0.2759	-0.0889	-0.3863
		0.3750	0.2375		0.2336	-0.2010	0.0704	-0.1669	-0.2422
Ciano		-0.1367	-0.5357	0.1792	-	0.4877	-0.2361	-0.1093	-0.2982
		-0.2033	0.2167	-0.1958		0.3607	-0.5536	0.1346	-0.3494
Inia		0.2042	-0.0013	-0.2167	0.6943	-	-1.0213	0.8781	-0.1550
		0.2448	0.0412	-0.0958	0.1668		-1.0940	1.0251	-0.1799

Reciprocal effects

TABLE 50. Number of spikelets per spike

Marquis		-	0.3819	0.2495	-0.0846	-0.3061	0.8035	0.6124	-0.0831
			0.1083	0.4159	0.0875	-0.0067	0.6312	0.3646	-0.0845
Chinook		-0.0993	-	0.1926	-0.0259	-0.1115	0.2629	0.0359	-0.0345
		0.0138		-0.3419	0.2164	0.1788	0.2373	0.0215	-0.0805
Khush-hal		0.4042	-0.1623	-	0.1214	-0.0359	-0.4382	0.1588	-0.0500
		0.1975	-0.1708		0.0086	0.0971	-0.3260	0.0725	0.0122
Ciano		-0.2898	-0.1850	0.0875	-	0.0676	-0.5110	0.2279	-0.0756
		0.1233	0.2027	0.1573		-0.1626	-0.5021	0.2183	-0.0663
Inia		0.0335	0.0988	0.1557	0.1650	-	-0.1172	-0.0195	-0.0457
		0.3435	0.3020	0.0598	-0.0790		-0.0404	-0.0322	-0.0618

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 51. Number of seeds per spike

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.1015	0.0655	0.4011	-1.3428	3.5835	12.0552	-1.9664
			0.2519	0.1132	0.8717	0.3590	2.0422	3.7491	-1.0532
Chinook		0.1910	-	-0.3113	0.0544	0.0701	-1.8660	2.6953	-1.9630
		-0.6400		-1.5280	0.2122	1.3177	-1.2955	1.2570	-1.0321
Khush-hal		0.8403	-0.7640	-	-0.9921	0.2122	-1.1196	0.4670	-1.9327
		0.7335	0.4013		-0.8981	0.0125	0.5107	-0.1605	-0.2707
Ciano		-1.1300	-1.0005	-0.5227	-	1.8083	-2.1986	4.0471	-1.5837
		0.7405	0.4957	1.0112		-0.2557	-2.4295	5.4813	-0.5161
Inia		-0.4867	0.0820	-0.2068	-1.2177	-	1.6006	1.7754	-0.2588
		0.3572	0.0558	0.3265	-0.5962		1.1722	0.9527	-0.4097

Reciprocal effects

TABLE 52. Weight of seeds per spike

Marquis		-	0.0490	-0.0080	-0.0624	-0.0289	-0.0059	-0.0029	-0.0074
			0.0461	-0.0314	0.0606	0.0699	-0.0342	-0.0004	-0.0039
Chinook		0.0552	-	-0.0406	-0.0150	-0.0264	-0.1185	0.0111	-0.0066
		0.0048		-0.0746	0.0018	0.0180	-0.0813	0.0050	-0.0032
Khush-hal		0.0022	-0.0190	-	0.0007	0.0178	-0.0222	-0.0025	-0.0068
		0.0150	0.0120		-0.0103	-0.0050	0.0577	0.0018	-0.0017
Ciano		-0.0810	-0.0268	-0.0028	-	0.0589	-0.0306	-0.0020	-0.0068
		0.0340	0.0335	0.0553		-0.0137	-0.0309	-0.0006	-0.0027
Inia		-0.0638	0.0252	-0.0277	-0.0853	-	0.1771	0.0284	-0.0056
		-0.0573	-0.0090	0.0240	-0.0190		0.0888	0.0063	-0.0021

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set set at two locations.

TABLE 53. 1000-kernel weight

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.6721 0.8088	-0.3252 -0.7960	-0.8322 0.4879	0.3192 1.4128	-2.6314 -2.3445	6.4507 5.0647	-1.1837 -1.0796
Chinook		0.9477 0.4982	-	-0.5640 -0.5859	-0.4496 -0.1117	-0.4911 -0.5019	-1.2960 -0.7879	1.2062 0.1889	-1.0332 -0.8615
Khush-hal		-0.5490 -0.1602	0.3412 0.0255	-	0.5533 0.8728	0.3476 -0.0248	0.3155 0.9186	-0.3740 0.4120	-1.0425 -0.7540
Ciano		0.5182 0.4008	0.1213 0.3108	0.5002 -0.0305	-	-0.5193 -0.1230	1.4580 1.4448	1.6523 1.6556	-0.7835 -0.7422
Inia		-0.8622 -1.3710	0.5862 -0.2628	-0.1982 0.2245	-0.7360 -0.0462	-	2.1540 0.7690	4.1662 0.1496	-0.9392 -0.3250

Reciprocal effects

TABLE 54. Yield per plant

Marquis		-	0.5268 0.6335	0.1073 -0.0471	-0.2387 -0.3599	-0.6415 0.0177	0.0570 -0.4831	-0.3228 0.0377	-0.8150 -0.4891
Chinook		0.7010 -0.4425	-	0.6673 -0.6144	-0.0782 -0.2531	-0.6920 0.0680	-0.7077 0.2577	0.1748 -0.1292	-0.7225 -0.3553
Khush-hal		0.3322 0.1092	-0.1002 0.6103	-	0.2599 0.5103	-1.2433 -0.7849	-0.6801 -0.0136	0.1365 -0.1995	-0.6627 -0.3625
Ciano		-0.3313 0.5293	-0.8415 0.0917	0.7498 0.6003	-	0.3511 0.0547	0.3461 -0.0030	-0.2062 -0.1956	-0.7715 -0.3378
Inia		-0.6825 -0.8422	0.2547 0.7200	-0.4963 0.0107	1.1603 0.1920	-	0.9848 0.2419	0.6438 -0.1371	0.0374 -0.2811

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

TABLE 55

Analysis of variance of general and specific combining ability and reciprocal effects for ten characters from backcross diallel set at two locations.

Character	M.S. for GCA	M.S. for SCA	M.S. for reciprocal effects	Error M.S.
Onset-of-heading	22.1406**	2.5500**	0.1059	0.2363
	32.1406**	2.3875**	0.2753	0.5273
Final heading	36.8594**	1.7687**	0.1462	0.1901
	39.1250**	3.8375**	0.3823	0.6637
Heading-span	2.3482**	0.5423*	0.0976	0.2164
	2.9344**	1.2388	0.2347	0.7498
Plant height	1263.1875**	13.8687**	10.2239	5.1350
	1345.4687**	26.5062**	6.8296	7.2887
Number of tillers per plant	4.3223**	0.3368	0.2838	0.6138
	7.3193**	0.9020	0.0941	0.6445
Number of spikelets per spike	2.9551**	0.1430	0.0776	0.1247
	2.0391**	0.1289	0.0736	0.1266
Number of seeds per spike	62.4219**	1.6523	1.1293	2.9885
	33.4844**	2.1719	0.7036	1.5811
Weight of seeds per spike	0.1172**	0.0032	0.0047	0.0110
	0.0499**	0.0078	0.0020	0.0058
1000-kernel weight	38.6875**	0.8004	0.7034	1.7762
	24.1055**	1.5766	0.5068	1.6191
Yield per plant	5.1455**	1.2141	0.7258	1.2218
	0.9004	0.5074	0.5015	0.7331

First reading under each column refers to Ellerslie and the second to Parkland.
* Significant at 5% level
**Significant at 1% level

In yield per plant (Table 54), cross (MxCH) had the highest SCA and consequently was the highest yielding at both locations, while cross (KxI) was the lowest yielding as it had the lowest SCA. The highest yielding hybrid had the parents (Marquis at Parkland and Chinook at Ellerslie) with the lowest GCA, while the poor yielding cross (KxI) had one parent (Khush-hal) with the lowest and one (Inia) with the highest GCA at both locations. The GCA variances were higher than those for SCA only for Marquis at Parkland and Chinook, Khush-hal and Inia at Ellerslie. The reciprocal effects were non-significant in all cases.

The analysis of variance for general and specific combining ability together with the reciprocal effects (Table 55) reveals important additive gene effects for all the characters at both locations, with the exception of yield per plant at Parkland. Thus the significance of mean squares for GCA's substantiates the differences among the parental lines. The significant mean squares for SCA's for onset-of-heading, final heading and plant height at both locations and heading-span at Ellerslie suggest a relatively greater importance of SCA over GCA. Thus for earliness and plant height, selection for SCA should be given priority in breeding programmes aimed at evolving desired lines.

Diallel cross analysis

Preceding the analysis, the validity of the assumption of no reciprocal differences was tested by means of Hayman's (1954a) analysis of variance. The results are given in Table 56. Heading-span at Ellerslie and plant height at Parkland showed a significant

TABLE 56

Mean squares from the analysis of variance
of 5 x 5 backcross diallel set for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Final heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
a	4	66.5313**	110.6094**	7.0449**	3790.0000**	12.9570*	8.8652**	187.3125**	0.2514*	115.9844**	15.4229**
		96.3906**	117.4531**	8.8047*	4037.0000**	21.9541**	6.1113*	100.3906**	0.1495*	72.2969**	2.6934
b	10	7.6625**	5.3062	1.6266	41.5000*	1.0152	0.4316	5.0000	0.0038	2.4312	3.6477
		7.1937**	11.5375**	3.7156	79.3000*	2.7094	0.2918	6.5812	0.0234	4.7312	1.5289
b_1	1	27.4519	19.3802*	0.1302	4.8411	0.0016	0.5952	0.0135	0.0091	4.9872	2.8834
		45.4352	59.8419	3.0000	5.6988	14.0152	1.0854	0.6248	0.0113	6.2116	1.8030
b_2	4	4.5937*	1.3437	2.8215	33.0156	1.2312	0.6533	4.7842	0.0036	1.3271	5.6904
		3.8926	7.8437	6.3035	120.1719	2.6053	0.2109	12.2314	0.0489	5.3594	1.1279
b_3	5	6.1500**	5.6250**	0.9711	55.6125	1.0469	0.2281	6.2000	0.0149	2.8000	2.1734
		2.1875	2.8375	1.7891*	61.6000**	0.5344	0.4039*	3.2625	0.0055	3.9750**	1.7984
c	4	0.2365	0.2542	0.4969*	46.9064	0.6718	0.1605	2.9725	0.0112	1.5768	1.0532
		1.1062	0.7573	0.8417	18.1423*	0.4849	0.3921	3.6308	0.0083	1.0007	1.4769
d	6	0.3719	0.5615	0.1566	19.8087	0.9712	0.2808	3.6648	0.0160	2.4660	2.9268
		0.6392	1.4066	0.6125	22.0532	0.1470	0.1070	1.0973	0.0045	1.8668	1.5227
Blocks x a	8	1.1953	0.6484	0.8697	14.9219	2.4395	0.9517	17.9219	0.0558	11.2734	1.6191
		1.5703	2.3578	2.5236	38.5859	2.3799	0.8940	8.5703	0.0238	4.4165	3.7525
Blocks x b	20	0.9625	0.8375	0.8468	19.8469	2.4242	0.2797	8.5250	0.0360	6.3781	5.4461
		1.9500	3.5156	3.5536	28.0469	2.5652	0.4021	5.3062	0.0257	7.2645	2.5219
Blocks x b_1	3	0.3767	0.9554	1.5654	13.4377	3.3930	0.8469	31.8310	0.0879	4.1877	16.2239
		9.2654	25.2762	5.1350	217.9666	25.4726	0.0840	0.5820	0.0585	17.8517	0.1980
Blocks x b_2	8	0.9814	0.8145	1.0515	26.3594	4.8573	0.2700	9.7495	0.0580	13.1274	7.6065
		1.8823	3.8979	7.5664	33.3281	2.5774	0.8656	11.6685	0.0530	15.1216	4.5089
Blocks x b_3	10	0.5062	0.9438	0.6952	17.3562	0.6228	0.2527	6.0667	0.0167	1.8535	3.1770
		1.4375	1.8312	0.5326	7.5562	0.5187	0.9073	1.2094	0.0032	0.6453	1.4113
Blocks x c	8	0.2918	0.2979	0.1000	13.7981	0.9417	0.1508	5.0430	0.0118	1.5511	3.5782
		1.3125	0.3069	0.9120	4.0308	1.9616	0.2277	3.6050	0.0098	5.2596	1.8341
Blocks x d	12	0.2427	0.2771	0.5253	9.5492	1.1389	0.2996	5.9260	0.0276	2.1627	2.1360
		1.1632	0.3981	0.7644	12.6719	0.5689	0.1085	2.0342	0.0053	0.9139	0.8813
Error	48	0.7079	0.5759	0.6491	15.4430	1.8594	0.3752	8.8616	0.0332	5.3357	3.6694
		1.5838	1.9922	2.2514	21.9569	1.9246	0.3817	4.7487	0.0176	4.8681	2.2023

* Significant at 5% level
**Significant at 1% level
First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of (a-b-c-d)
Each component has been tested against its own block interaction.

TABLE 57

Analysis of variance of $W_p + V_p$ for ten characters from backcross diallel set at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.
Onset-of-heading	4.9320	1.5831*	0.3734
	16.4215	1.6003*	0.8179
Final heading	0.2722	0.7315*	0.1721
	38.3562	2.5496	1.9131
Heading-span	0.5333	0.0653	0.2201
	1.1121	0.7220	1.1063
Plant height	12060.9687	309.5469	329.9219
	9119.5000	303.1406*	77.2656
Number of tillers per plant	6.5381	0.4283	0.7682
	1.0551	0.6511	0.8967
Number of spikelets per spike	0.3622	0.0215	0.0076
	0.0270	0.0133	0.0426
Number of seeds per spike	426.5688	9.7215	13.6923
	54.6648	3.2239	4.9508
Weight of seeds per spike	0.0049	0.0002	0.0002
	0.0021	0.00	0.00
1000-kernel weight	295.2457	2.3595	3.4383
	38.0292	1.3192	4.0242
Yield per plant	6.7847	1.9057	2.6477
	0.2112	0.7162	0.9051

First reading under each column refers to Ellerslie and second to Parkland.
*Significant at 5% level

TABLE 58

Estimates of second degree statistics for ten characters from backcross diallel set at two locations.

Character	V_{OLD}	W_{OLOT}	V_{OLL}	V_{ILL}	$(M_{L1} - M_{L2})^2$
Onset-of-heading	15.0000	5.7395	2.2227	3.4973	1.4641
	15.7002	6.6334	3.2148	4.4137	2.4233
Final heading	16.9668	7.8656	3.6934	4.5766	1.0336
	27.1514	10.1422	3.9199	5.8430	3.7249
Heading-span	0.5889	0.2610	0.2349	0.5060	0.0069
	3.6111	0.8947	0.2936	0.9129	0.1600
Plant height	486.7740	246.3824	126.3408	133.2646	0.2528
	518.4434	258.1760	134.5703	147.5088	0.3040
Number of tillers per plant	1.4343	0.7289	0.4319	0.6010	0.0008
	5.4749	1.9703	0.7317	1.1834	0.7475
Number of spikelets per spike	1.2283	0.5699	0.2957	0.3676	0.0317
	0.5749	0.3369	0.2039	0.2692	0.0578
Number of seeds per spike	28.9980	13.2521	6.2422	7.0721	0.0007
	12.2275	5.7904	3.3457	4.4383	0.0333
Weight of seeds per spike	0.0384	0.0211	0.0117	0.0133	0.0004
	0.0360	0.0116	0.0050	0.0089	0.0006
1000-kernel weight	16.7744	7.9937	3.8662	4.2670	0.2660
	13.1670	5.4328	2.4092	3.1975	0.3312
Yield per plant	5.4558	1.5937	0.5142	1.1225	0.1538
	0.8875	0.2552	0.0899	0.3447	0.0961

First reading under each column refers to Ellerslie and second to Parkland.

c component, indicating significant reciprocal differences. Significance for a confirms the existence of parental differences for all characters at both locations, with the exception of yield per plant at Parkland. Significance of b shows that dominance is present for onset-of-heading, final heading and plant height at both locations while b_1 shows that dominance is directional for final heading at Ellerslie. Other assumptions underlying the diallel analysis were tested by analysis of variance of $W_r - V_r$ differences. The heterogeneity of $W_r - V_r$ over arrays for onset-of-heading and heading-span at Ellerslie and plant height at Parkland (Table 57) indicates non-validity of at least one of the assumptions: no multiple allelism, uncorrelated gene distribution and no non-allelic gene interaction. This situation is discussed later, during the graphical analysis of these characters.

The estimates of second degree statistics calculated from array variances and parent-offspring covariances are presented in Table 58. The genetic components of variation were computed according to Johnson and Aksel's (1959) procedure, where the effects of heterozygote is halved because the backcross entries were made equal to those of F_2's (Jinks, 1956). The estimates of genetic components of variation are given in Table 59. Significance was tested in a manner similar to that used for F_2's. Proportional estimates of genetic parameters, calculated from Table 59 are presented in Table 60. The interpretation of the results in Tables 59 and 60, together with, the graphical analysis of the data for all the characters under study is as follows:

Except E at Ellerslie and F at Parkland, all components

TABLE 59

Estimates of genetic components of variation
from backcross diallel set for ten characters at two locations.

Character	D	F	H_1	H_2	h	E
Onset-of-heading	14.7635 ± 0.5161**	6.7593 ± 1.2092**	5.4162 ± 1.3938**	4.6253 ± 1.2642**	5.7051 ± 0.8535**	0.2364 ± 0.2107
	13.9224 ± 0.5422**	1.7335 ± 1.3543	4.1991 ± 1.4642**	3.7397 ± 1.3280**	9.3953 ± 0.8966**	0.5278 ± 0.2213*
Final heading	16.7767 ± 0.4081**	2.2630 ± 1.2193	3.3163 ± 1.3182**	3.1526 ± 1.1956**	4.0130 ± 0.8072**	0.1901 ± 0.1993
	25.8080 ± 0.1919**	11.5783 ± 0.4993**	7.5494 ± 0.5393**	6.3649 ± 0.4896**	14.4746 ± 0.3305**	0.6636 ± 0.0816**
Heading-span	0.3726 ± 0.2020*	-0.0456 ± 0.5045	1.0865 ± 0.5455*	0.6157 ± 0.4947	-0.1107 ± 0.3340	0.2164 ± 0.0829**
	2.9149 ± 0.4003**	3.8513 ± 1.2247*	1.7867 ± 1.3240	0.9762 ± 1.2009	0.1597 ± 0.8106	0.7505 ± 0.2001**
Plant height	481.6387 ± 6.3195**	-18.1412 ± 15.7872	20.9514 ± 17.0677	17.4245 ± 15.4806	-2.2534 ± 10.4517	5.1354 ± 2.5801**
	511.1506 ± 11.9086**	-4.5084 ± 29.7476	58.0338 ± 32.1602	38.3688 ± 29.1700	-3.4512 ± 19.6940	7.2925 ± 4.8716
Number of tillers per plant	0.8154 ± 0.0969**	-0.7879 ± 0.2422**	-0.6063 ± 0.2618**	-0.5614 ± 0.2375*	-0.3957 ± 0.1603**	0.6189 ± 0.0396**
	4.8305 ± 0.1501**	2.2954 ± 0.3750**	0.6520 ± 0.4054	0.5180 ± 0.3677	2.5775 ± 0.2482	0.6444 ± 0.0613**
Number of spikelets per spike	1.1017 ± 0.0589**	0.0273 ± 0.1472	0.0948 ± 0.1591	0.0382 ± 0.1443	0.0472 ± 0.0975	0.1246 ± 0.0241**
	0.4482 ± 0.0313**	-0.3498 ± 0.0782**	-0.0253 ± 0.0845	0.0080 ± 0.0767	0.1504 ± 0.0518**	0.1267 ± 0.0128**
Number of seeds per spike	26.0484 ± 0.7304**	1.4479 ± 1.8244	-3.3914 ± 1.9724	-2.5798 ± 1.7890	-1.8849 ± 1.2078	2.9497 ± 0.2982**
	10.6477 ± 0.6544**	-0.6025 ± 1.6346	2.7113 ± 1.7672	1.2106 ± 1.6028	-0.8779 ± 1.0822	1.5799 ± 0.2671**
Weight of seeds per spike	0.0273 ± 0.0007**	-0.0210 ± 0.0017**	-0.0215 ± 0.0019**	-0.0156 ± 0.0017**	-0.0051 ± 0.0011**	0.0111 ± 0.0003**
	0.0302 ± 0.0017**	0.0188 ± 0.0044**	0.0101 ± 0.0047**	0.0038 ± 0.0043	-0.0014 ± 0.0029	0.0059 ± 0.0007**
1000-kernel weight	14.9088 ± 0.1177**	-0.5569 ± 0.2940	-2.7402 ± 0.3178**	-1.9481 ± 0.2882**	-0.0724 ± 0.1946	1.7756 ± 0.0480**
	11.5476 ± 0.3657**	2.6595 ± 0.9136**	0.0153 ± 0.9877	-0.0656 ± 0.8958	0.2886 ± 0.6048	1.6194 ± 0.1493**
Yield per plant	4.2333 ± 0.3936**	3.0700 ± 0.9832**	0.3925 ± 1.0630	-0.0118 ± 0.9642	-0.1673 ± 0.6509	1.2225 ± 0.1607**
	0.1536 ± 0.1558	-0.1264 ± 0.3892	-0.6622 ± 0.4208	-0.4481 ± 0.3817	-0.0849 ± 0.2577	0.7336 ± 0.0631**

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
**Significant at 1% level

TABLE 60

Proportional estimates of genetic parameters
from the backcross diallel set for ten characters at two locations.

Character	$[H_1/D]^{\frac{1}{2}}$	$[H_2/4H_1]$	$\{(4DH_1)^{\frac{1}{2}}+F\} \div \{(4DH_1)^{\frac{1}{2}}-F\}$	h^2/H_2	$r_{y_r/W_r + V_r}$	Heritability
Onset-of-heading	0.6057*	0.2135*	2.2149*	1.2334	0.9758	1.0275
	0.5492*	0.2227*	1.2557*	2.5016	0.9398	0.7527
Final heading	0.4446*	0.2377*	1.3539*	1.2729	0.9486	0.9003
	0.5409*	0.2108*	2.4173*	2.2741	0.9672	1.0562
Heading-span	1.7077*	0.1500	0.9305†	-0.1699	0.6344	0.1571
	0.7829	0.1366	4.3292	0.1636	0.4387	0.6007
Plant height	0.2086	0.2079	0.8343	-0.1293	0.3243	0.8898
	0.3369	0.1653	0.9738	-0.0899	-0.6073	0.8477
Number of tillers per plant	0.9174	0.2045	0.3090	0.7049	0.8415	0.2403
	0.3674	0.1986	4.6612	4.9754	0.9151	0.8379
Number of spikelets per spike	0.2931	0.1007	1.0880	1.2373	-0.5694	0.9423
	0.2375	-0.0787	-0.2433	18.8908	-0.8324	0.3502
Number of seeds per spike	0.3608	0.1902	1.1669	0.7306	-0.5376	0.7891
	0.5046	0.1116	0.8938	-0.7552	0.2682	0.5250
Weight of seeds per spike	0.8884	0.1814	0.3949	0.3291	-0.1965	0.3834
	0.5775*	0.0946	3.3493*	-0.3582	0.3449	0.6696
1000-kernel weight	0.4281	0.1772	0.9169	0.0371	0.5993	0.7533
	0.0364	-1.4023	-1.9226	-3.3718	-0.4941	0.7507
Yield per plant	0.3045	-0.0075	-11.4843	14.1870	0.9215	0.6567
	2.0749	0.1692	0.6694	0.1894	-0.4361	0.0602

First reading under each column refers to Ellerslie and second to Parkland.
*Genetic components of variation for the characters are significantly different from zero ($P \leq 0.05$)
†Components D and H_1 significant, F non-significant ($P > 0.05$)

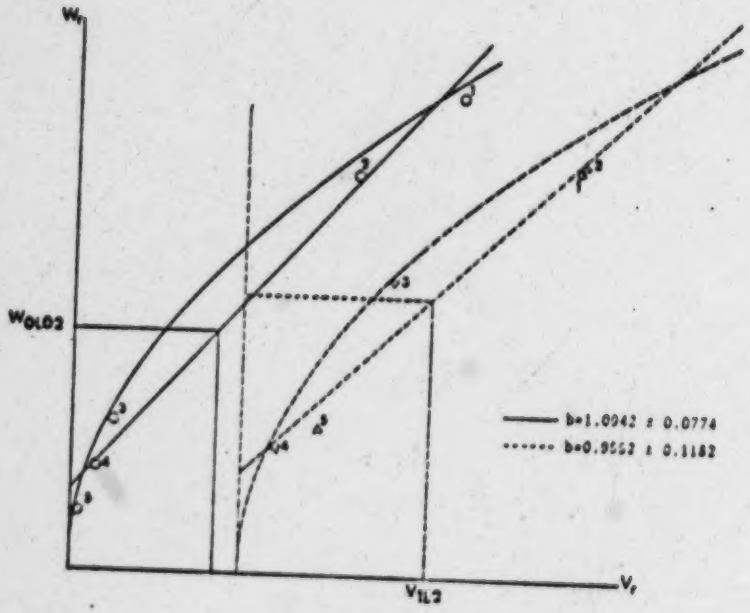

Figure 41. W_r, V_r graph for onset-of-heading from backcross diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

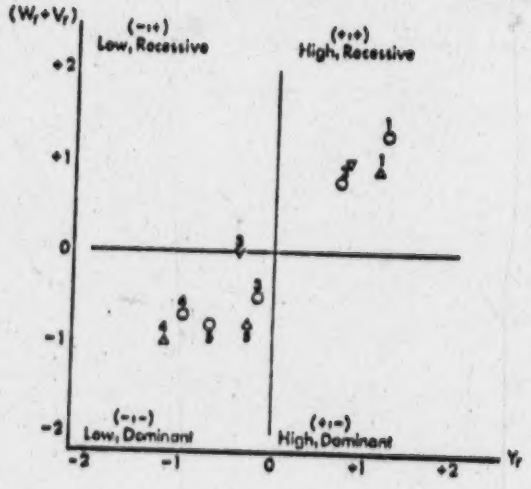

Figure 42. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from backcross diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

of variation were significant (Table 59) for onset-of-heading. The mean degree of dominance (Table 60) and the regression of W_r upon V_r (Figure 41) at both locations show that onset-of-heading is inherited as a partially dominant trait. The proportion of positive to negative alleles at loci exhibiting dominance in the parents is approximately 0.25 and consequently the parents may be assumed to have equal proportions of genes with positive and negative effects respectively. The estimates of $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F] > 1$ for both locations suggest that dominant genes are in excess in the parents. Moreover, since h^2/H_2 is 1.2 for Ellerslie and 2.5 for Parkland, at least one and at least two groups of genes, respectively, are showing dominance in regard to the expression of the character. The correlation coefficient between Y_r and $(W_r + V_r)$ at both locations is 0.9, indicating that the genes for early heading are mostly dominant. The parents Marquis and Inia at Ellerslie and Chinook and Ciano at Parkland are the most highly recessive and highly dominant ones (Figure 41). The standardized deviation graph of Figure 42 categorized the late heading parents as recessives (Marquis and Chinook, in the +,+ quadrant) and the early parents as dominants (Khush-hal, Ciano and Inia, in the -,- quadrant) for both locations. Heritability estimates of 102.75% at Ellerslie and 75.27% at Parkland show that the character is highly heritable and fairly stable over the environmental fluctuations.

Only F and E for final heading were not significant at Ellerslie (Table 59). The character is partially dominant in its inheritance since $(H_1 \div D)^{1/2} < 1$ (see also Figure 43). Table 57 shows $W_r - V_r$

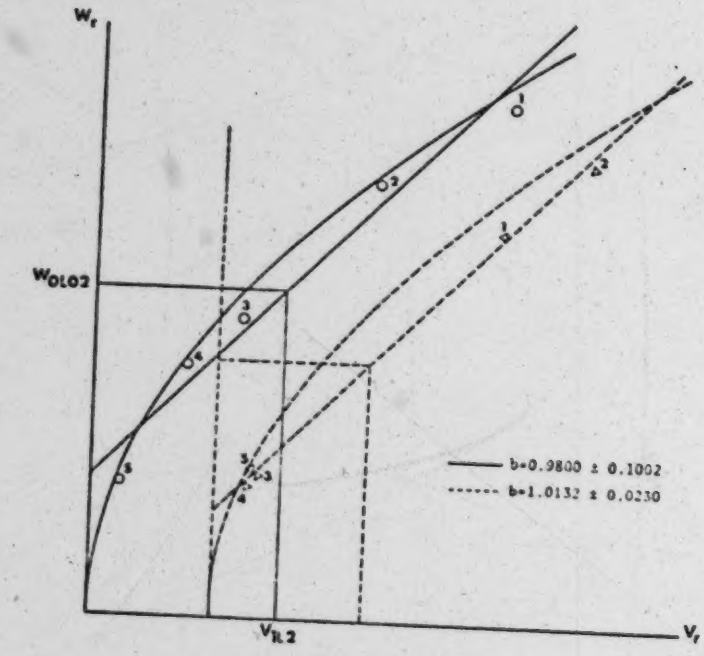

Figure 43. W_r, V_r graph for final heading from backcross diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

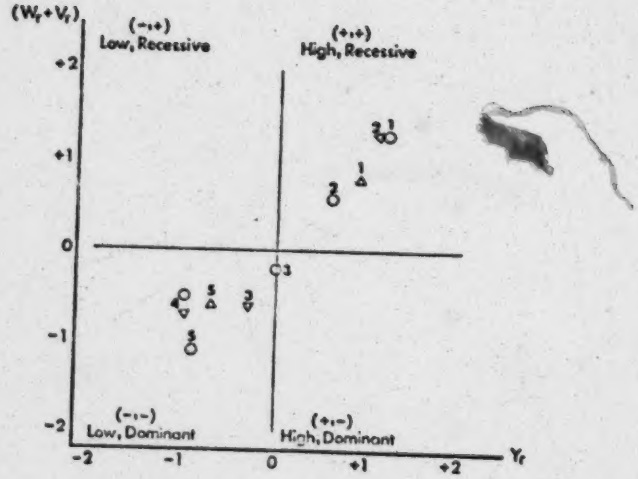

Figure 44. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from backcross diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

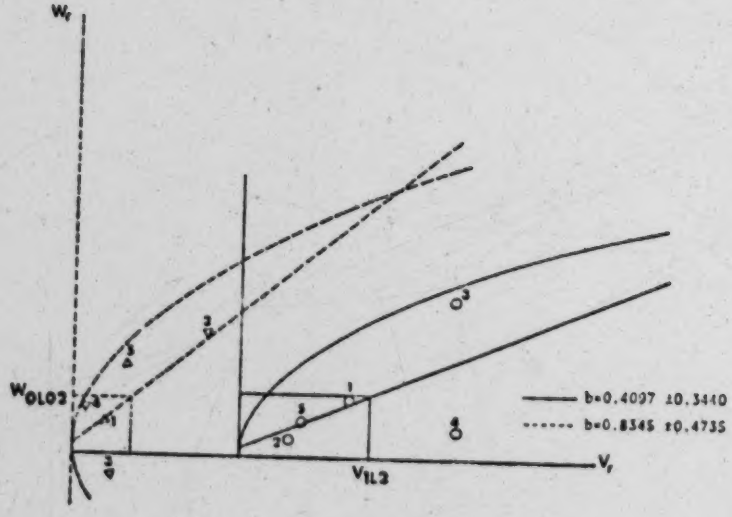

Figure 45. W_r, V_r graph for heading-span from backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

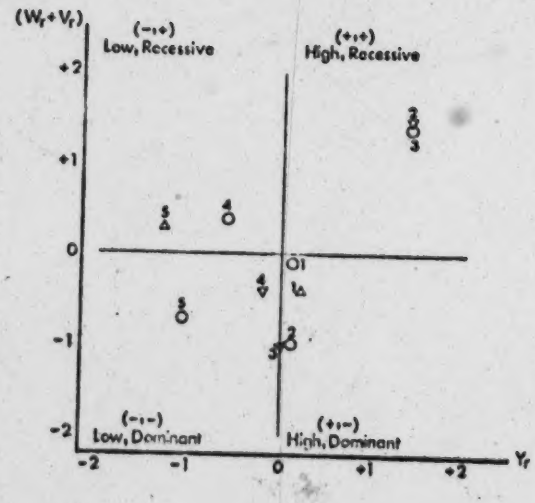

Figure 46. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

heterogeneity which can be ascribed to either non-allelic interaction, multiple allelism or correlated gene distribution. It could be ascertained from Figure 41 (onset-of-heading) and Figure 43 (final heading) that the regression line does not deviate significantly from the expected unit slope and the W_r, V_r graph does not appear to be distorted. Therefore the question of non-validity of any of the above mentioned conditions has been ignored. The general conclusions of the diallel analysis for final heading (see Tables 59, 60; Figures 43, 44) and heading-span (see Figure 45, 46) are similar to that for onset-of-heading except for changes in the ranking order of parents for their dominance.

For plant height, all components of genetic variation except D were non-significant at both locations. The $W_r - V_r$ heterogeneity at Parkland (Table 57) has been ignored, since the regression of W_r upon V_r is not significantly different from unity (Figure 47) and the W_r, V_r array-intercepts do not show distortion. Because of the non-significance of components of variation, interpretations of proportional estimates and genetic parameters are meaningless. However, the mean degree of dominance may be given as $(H_1 \div D)^{1/2} < 1$ indicating partial dominance (see also Figure 47). The correlation between the parental order of of dominance and parental measurements is 0.32 at Ellerslie and -0.607 at Parkland. The positive correlation at Ellerlie indicates that genes for shortness are mostly dominant; the negative correlation at Parkland that genes for tallness are mostly dominant. The most highly recessive parent (+,+ quadrant, Figure 48) contributing to tallness at Ellerslie is Marquis, while Khush-hal is the most highly recessive parent at Parkland

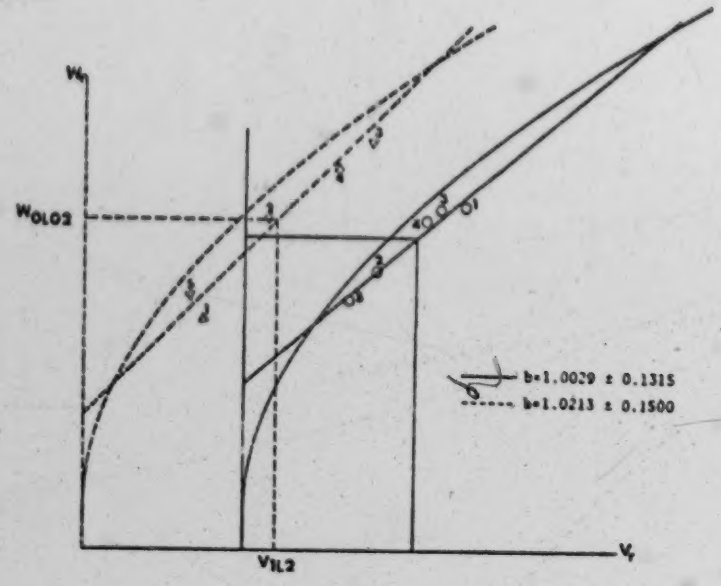

Figure 47. W_r, V_r graph for plant height from backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

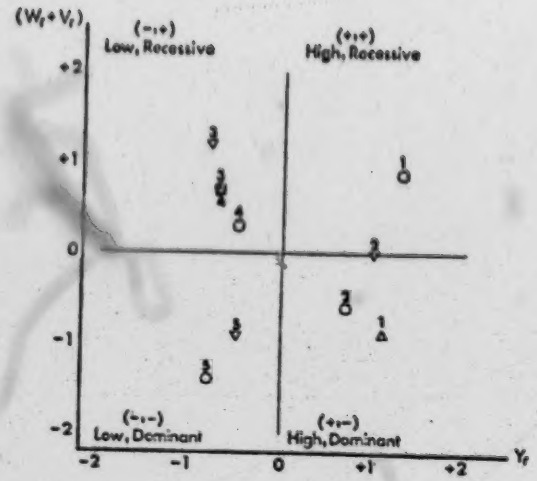

Figure 48. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

(-,+ quadrant) contributing to shortness. The most dominant parent, Inia, at both locations occupies the (-,-) quadrant and thus reflects its shortness. Marquis and Chinook show a discrepancy in dominance ranking order between locations. Chinook, highly dominant at Ellerslie had equal proportion of dominants and recessives at Parkland, while Marquis, highly recessive at Ellerslie is highly dominant at Parkland. The heritability estimates of 88.98% at Ellerslie and 84.77% at Parkland suggests that plant height, being highly heritable is quite stable with respect to environmental changes.

For number of tillers per plant, all components of variation except D and F are non-significant at Parkland. Consequently, proportional values discussed below may have a value only in showing trends and not definite conclusions. The same condition applies to the interpretation of graphs. At Ellerslie, $(H_1 \div D)^{1/2} \approx 1$, showing that dominance is nearly complete (see also Figure 49). The value of $(H_2/4H_1) = 0.204$ indicates a certain degree of asymmetry of positive and negative alleles at loci exhibiting dominance. the proportion of dominant to recessive genes in the parents (0.309), indicates a preponderance of recessive genes. Since $h^2/H_2 = 0.704$, probably at least one group of genes controls tillering capacity. The correlation between parental order of dominance and parental measurements at both locations is 0.9, suggesting that genes with low tillering capacity are mostly dominant. This situation is presented graphically in Figure 50, where almost all the parents at both locations occupy

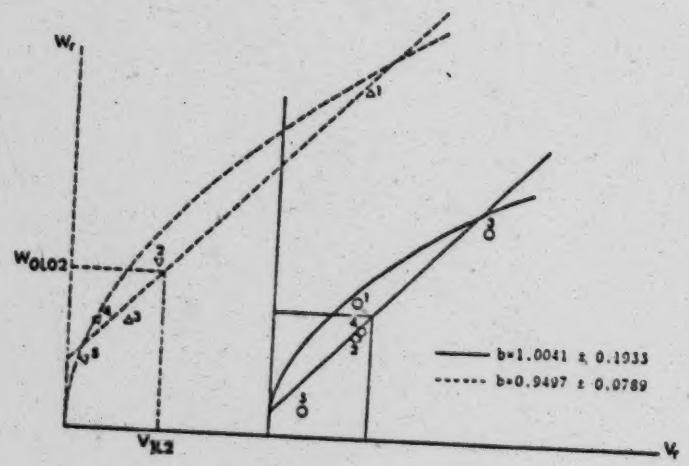

Figure 49. W_r, V_r graph for number of tillers per plant from backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

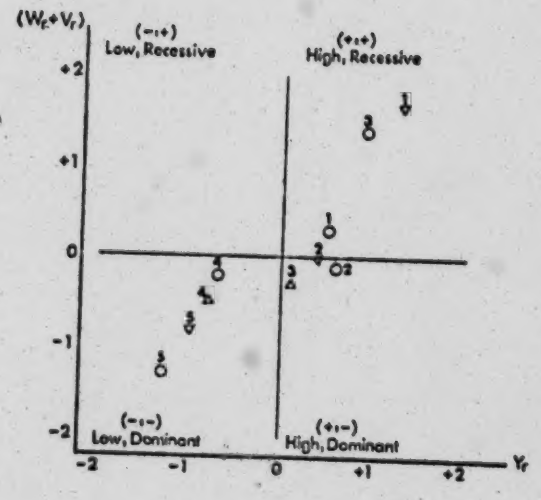

Figure 50. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

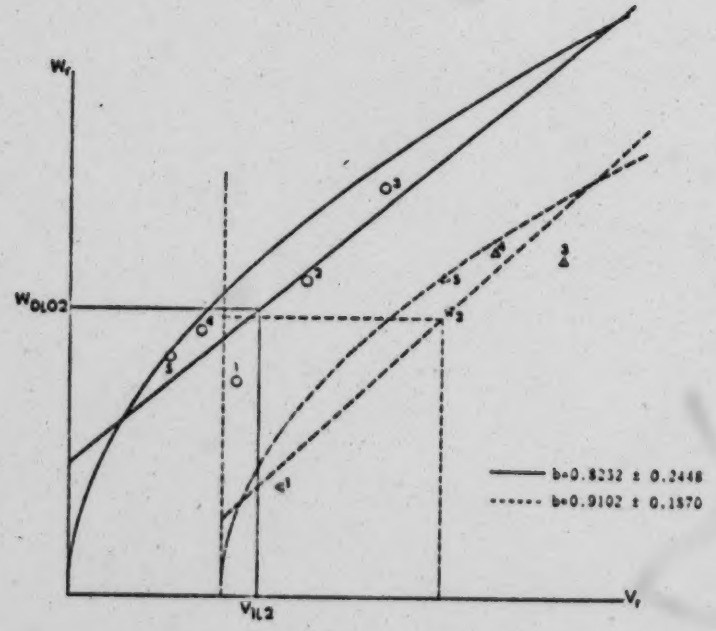

Figure 51. W_r, V_r graph for number of spikelets per spike from backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

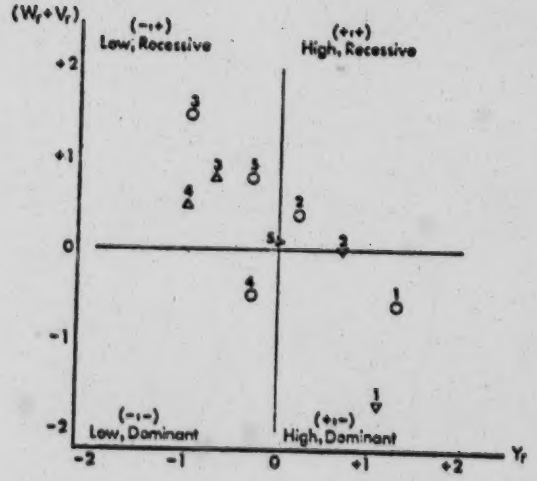

Figure 52. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

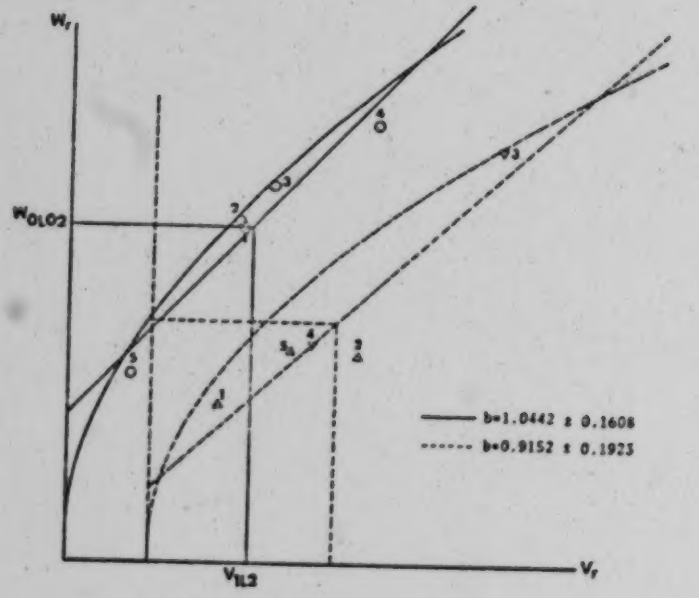

Figure 53. W_r, V_r graph for number of seeds seeds per spike from backcross diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

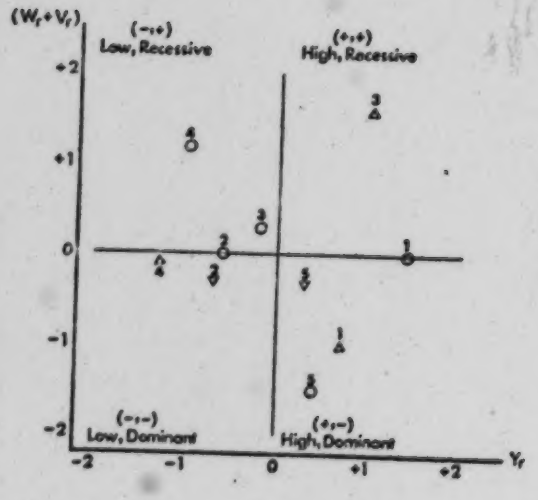

Figure 54. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from backcross diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

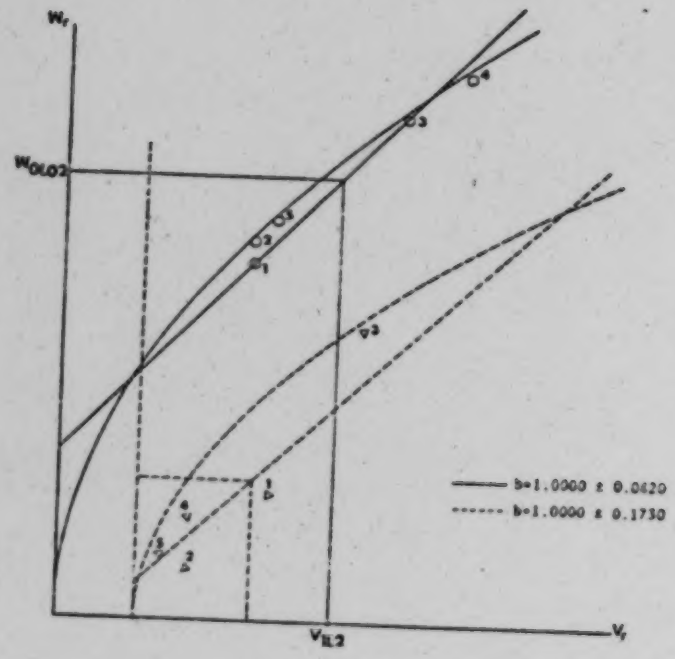

Figure 55. W_p, V_p graph for weight of seeds per spike from backcross diallel set.
—— o = W_p, V_p intercepts at Ellerslie
--- Δ = W_p, V_p intercepts at Parkland

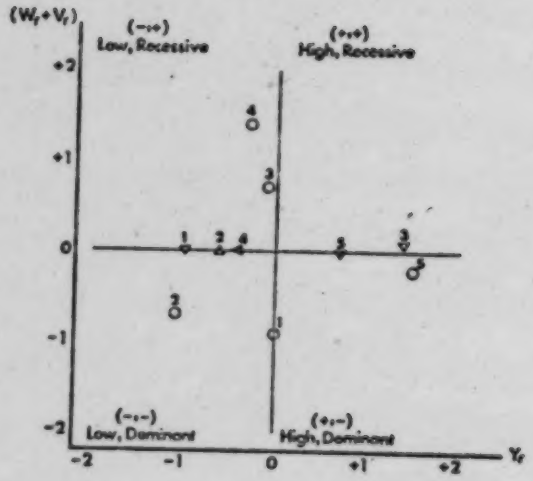

Figure 56. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for weight of seeds per spike from backcross diallel set.
o = Y_p, $[W_p + V_p]$ intercepts at Ellerslie
Δ = Y_p, $[W_p + V_p]$ intercepts at Parkland

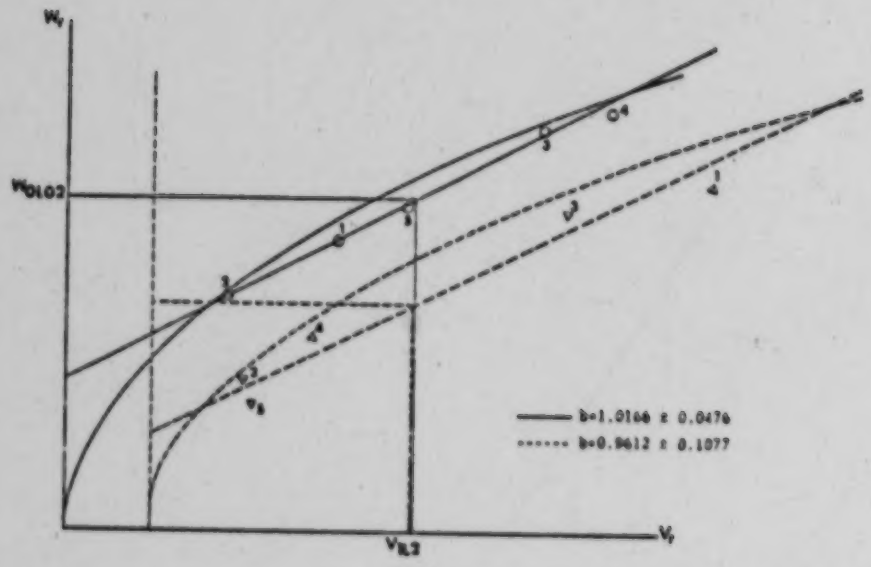

Figure 57. W_r, V_r graph for 1000-kernel weight from backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

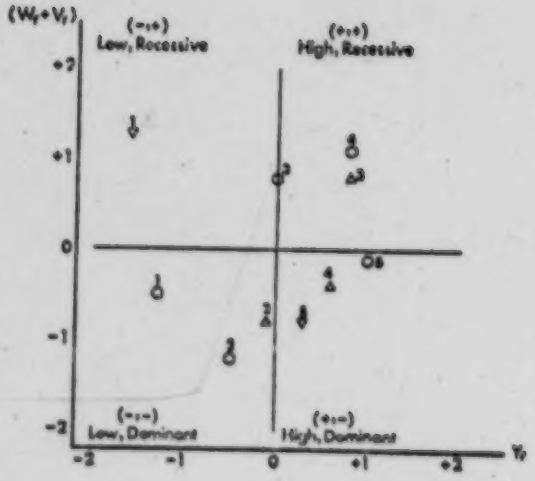

Figure 58. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

the (-,-) and (+,+) quadrants. Ciano and Inia, in the (-,-) quadrant, may be regarded as highly dominant for low tillering at both locations. Khush-hal at Ellerslie and Marquis at Parkland, in the (+,+) quadrant, may be said to be highly recessive for higher tillering. Chinook, with higher tillering capacity at both locations, shows more dominant than recessive genes at Ellerslie but equal proportions of dominants and recessives at Parkland. Only Khush-hal has changed its order of dominance between the two locations. Highly recessive at Ellerslie, it shows a preponderance of dominant genes at Parkland. Heritability values of 24.03% at Ellerslie and 83.79% at Parkland suggest that the heritability of tillering capacity is strongly influenced by environmental fluctuations.

The graphical interpretations of the results of Tables 59, 60 for other components of yield, are shown in Figures 51 - 58, (i.e. number of spikelets per spike, Figures 51, 52; number of seeds per spike, Figures 53, 54; weight of seeds per spike, Figures 55, 56; and 1000-kernel weight, Figures 57, 58). These may be explained in the same way as for number of tillers per plant.

For yield per plant, the components of variation in Table 59 were mostly non-significant. The overall picture of inheritance of yield seen from the W_p, V_p graph of Figure 59 is one of partial dominance at both locations. The correlations between parental order of dominance and parental measurements are 0.921 at Ellerslie and -0.436 at Parkland. These highly significant correlations indicate

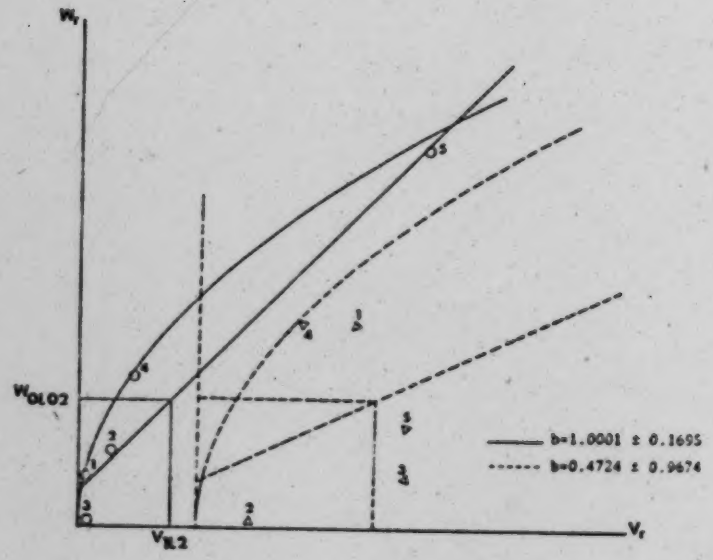

Figure 59. W_r, V_r graph for yield per plant from backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

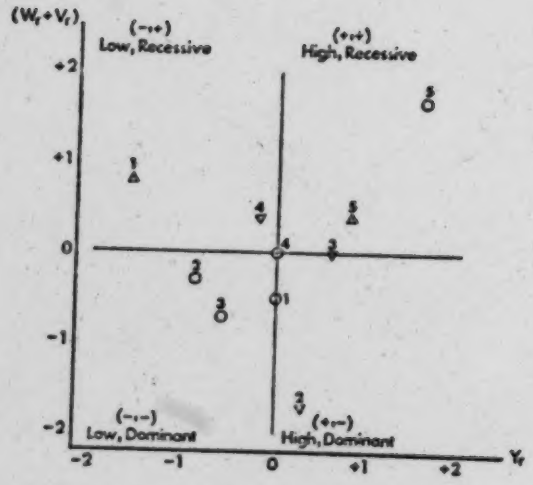

Figure 60. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

that the genes for low yield at Ellerslie are mostly dominant while at Parkland high yielding is dominant over low. The dominance ranking order of parents seems to be significantly different for the two locations. Thus, from Figure 59, Inia and Marquis are the most recessive and Khush-hal and Chinook are the most dominant parents at Ellerslie and Parkland, respectively. Marquis, highly recessive at Parkland contains an excess of dominant genes at Ellerslie, while Khus-hal, with equal proportion of dominants and recessives at Parkland shows a preponderance of dominants at Ellerslie. Ciano, with equal proportions of dominant and recessive genes at Ellerslie possesses an excess of recessive genes at Parkland. The heritability values of 65.67% at Ellerslie and 6.02% at Parkland reflect this instability of yield inheritance between the two locations.

ANALYSIS OF SELFED BACKCROSSES

In the absence of non-allelic interaction the expected statistics for the analysis of family means of the first selfed backcross generation are the same as those of F_3 generation crosses. The diallel table of selfed backcross family means, i.e., 'synthetic F_3 diallel table' was subjected to simple correlation analysis and the results are presented in Table 61. The following conclusions may be made from Table 61:

Onset-of-heading was positively correlated with final heading, plant height, number of spikelets per spike, number of seeds per spike at both locations and with number of tillers per plant at Parkland only. It was negatively correlated with weight of seeds per spike at Parkland and 1000-kernel weight at both locations. The negative correlation with weight of seeds per spike and 1000-kernel weight indicates that early maturing varieties produce higher yields and higher seed weights than the late maturing ones. Similar results were also obtained for F_1, F_2 and backcross diallel data.

Plant height was positively correlated with number of tillers per plant and number of spikelets per spike at both locations and with number of seeds per spike at Ellerslie only. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. Correlation with yield at both locations was not significant.

Number of tillers per plant was positively correlated with number of spikelets per spike and yield per plant at both locations

TABLE 61

Simple correlation coefficients between ten characters from a selfed backcross diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.917**	0.142	0.777**	0.194	0.534**	0.346**	-0.206	-0.643**	-0.206
	0.842**	0.047	0.818**	0.500**	0.534**	0.301**	-0.288*	-0.636**	-0.162
2. Final heading	-	0.515**	0.779**	0.197	0.445**	0.316**	-0.273*	-0.687**	-0.307**
		0.578**	0.771**	0.617**	0.527**	0.238*	-0.347	-0.656**	-0.009
3. Heading-span		-	0.259*	0.055	-0.081	-0.003	-0.275*	-0.330**	-0.349**
			0.191	0.390**	0.169	-0.011	-0.206	-0.254*	0.231*
4. Plant height			-	0.354**	0.636**	0.278*	-0.244*	-0.606**	0.016
				0.511**	0.588**	0.155	-0.465**	-0.723**	-0.103
5. Number of tillers per plant				-	0.285*	-0.056	-0.034	0.046	0.517**
					0.428**	0.239*	-0.255	-0.536**	0.253*
6. Number of spikelets per spike					-	0.619**	0.212*	-0.412**	0.252*
						0.686**	0.194	-0.345**	0.373**
7. Number of seeds per spike						-	0.695**	-0.302**	0.126
							0.639**	-0.061	0.409**
8. Weight of seeds per spike							-	0.526**	0.442**
								0.724**	0.511**
9. 1000-kernel weight								-	0.418**
									0.309**
10. Yield per plant									-

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
**Significant at 1% level

and with number of seeds per spike at Parkland. It was negatively correlated with 1000-kernel weight at Parkland. The correlation of tiller number with number of seeds per spike and 1000-kernel weight at Ellerslie and with weight of seeds per spike at both locations was not significant. A positive correlation with number of spikelets per spike, number of seeds per spike and yield per plant indicates a direct proportional relationship between tillering capacity and these characters, while negative correlation with 1000-kernel weight shows that plants with high tillering capacity tend to have a low kernel weight. The correlation coefficients for other components of yield, viz., number of spikelets per spike, number of seeds per spike and 1000-kernel weight among themselves and with heading dates have a similar interpretation.

Yield per plant was positively correlated with its components: 1000-kernel weight, weight of seeds per spike, number of seeds per spike, number of spikelets per spike and number of tillers per plant at both locations. The single exception was number of seeds per plant at Ellerslie. The positive correlation of yield with its components exhibits a direct proportional relationship of the former with the latter. Yield was negatively correlated with final heading and heading-span at both locations, indicating that the late heading entries are low yielding and vice versa. The negative correlation of yield with onset-of-heading was not significant at either location.

The results of the factor analysis are summarized in a varimax-rotated, five factor matrix in Table 62. 93% of the total

TABLE 62

Varimax rotated factor matrix for ten characters from a selfed backcross diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.982	0.977	0.057	-0.034	-0.025	0.147
	0.899	0.905	0.135	0.193	-0.005	-0.159
Final heading	0.985	0.908	0.036	-0.045	0.364	0.157
	0.956	0.766	0.078	0.241	0.520	-0.065
Heading-span	0.986	0.163	-0.078	-0.063	0.973	0.054
	0.991	0.086	-0.057	0.159	0.970	0.122
Plant height	0.850	0.787	0.010	0.266	0.166	0.383
	0.924	0.924	-0.079	0.348	0.053	0.017
Number of tillers per plant	0.877	0.246	-0.120	0.889	0.100	0.030
	0.898	0.344	0.079	0.817	0.227	0.234
Number of spikelets per spike	0.872	0.452	0.470	0.310	-0.158	0.572
	0.826	0.634	0.552	0.166	0.058	0.296
Number of seeds per spike	0.955	0.251	0.895	-0.060	0.030	0.293
	0.978	0.199	0.953	0.121	-0.011	0.122
Weight of seeds per spike	0.995	-0.206	0.899	0.138	-0.146	-0.332
	0.964	-0.325	0.749	-0.389	-0.112	0.366
1000-kernel weight	0.939	-0.534	0.126	0.261	-0.204	-0.727
	0.902	-0.581	0.115	-0.617	-0.139	0.388
Yield per plant	0.869	-0.232	0.281	0.817	-0.261	-0.018
	0.946	-0.066	0.298	0.085	0.140	0.908
Percent of total Variability explained	93.095	31.338	19.500	17.231	12.604	12.421
	92.841	33.077	19.144	14.301	13.203	13.115

First reading under each column refers to Ellerslie and second to Parkland.

variability present in the data for all the characters considered was explained by these factors at both locations.

The first factor was termed *lateness*. It carried highest loadings for onset-of-heading and final heading at both locations. Weight of seeds per spike, 1000-kernel weight and yield per plant were negative contributors to *lateness*. Of the remaining characters, the highest contributor to *lateness* was plant height at both locations. This confirms the results of the earlier F_1, F_2 and backcross diallel factor analyses. *Lateness* explained 31.33% and 33.07% of the total variability at Ellerslie and Parkland respectively.

The second principal factor was termed *yielding-ability* since it carried the highest loadings on number of seeds per spike, weight of seeds per spike and number of spikelets per spike. As expected, yield per plant appreciably contributed to this factor. The contributions of onset-of-heading and final heading, though positive, were the lowest. Heading-span and plant height showed a negative effect on *yielding-ability*. The factor explained 19% of the variability present in the data at both locations.

Tillering-capacity was chosen as the third principal factor as it carried the highest loadings for number of tillers per plant at both locations. Yield per plant showed the highest contribution to *tillering-capacity* at Ellerslie but its effect at Parkland was very low. Other components of yield, viz., number of seeds per spike, weight of seeds per spike and 1000-kernel weight, contributed negatively or very slightly to *tillering-capacity* at both locations. A negative effect

TABLE 63

Estimates of general combining ability for five parental lines used in selfed backcross diallel set for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	2.0733	1.2483	-0.5433	-1.6100	-0.0683
	2.3117	1.5534	-0.6300	-2.3216	-0.9133
Final heading	2.8616	1.4983	-0.2433	-2.0183	-1.5183
	2.1917	2.2334	-0.5500	-2.2250	-1.6500
Heading-span	0.1967	0.3717	0.2550	-0.4533	-0.3700
	-0.1033	0.6633	0.0967	0.0967	-0.7533
Plant height	14.0397	9.8603	-8.6035	-6.1142	-9.1824
	12.5270	12.5012	-8.7700	-7.7140	-8.5442
Number of tillers per plant	0.0554	0.5642	0.3819	-0.0788	-0.9226
	0.7212	0.7512	0.3558	-0.7265	-1.1017
Number of spikelets per spike	0.7318	0.1207	-0.4789	-0.2321	-0.1415
	0.5099	0.3313	-0.2941	-0.4894	-0.0577
Number of seeds per spike	3.7367	-2.1908	-1.2477	-1.6029	1.3047
	1.8352	-1.0805	0.4308	-1.8508	0.6653
Weight of seeds per spike	0.0230	-0.1290	-0.0362	-0.0017	0.1439
	-0.0314	-0.0845	0.0607	-0.0282	0.0834
1000-kernel weight	-2.3425	-1.1454	0.2488	1.4072	1.8379
	-2.0504	-1.0151	0.9964	0.9224	1.1968
Yield per plant	-0.0471	-0.8473	-0.7653	0.6451	1.0147
	0.5386	0.0681	0.3231	-0.2341	0.3815

First reading under each column refers to Ellerslie and second to Parkland.

was observed for onset-of-heading, final heading and heading-span at Ellerslie, but their effect at Parkland, though positive, was very low. *Tillering-capacity* explained 17.23% and 14.30% of the variability in the data at Ellerslie and Parkland.

The fourth principal component was chosen as *heading-span* because heading-span provided the highest contribution to this factor. It explained 12.6% and 13.2% of the variability at Ellerslie and Parkland. Yield per plant and its components had either a negative or a minimal effect on *heading-period*. This kind of response was also observed in the F_1, F_2 and backcross factor analyses.

The fifth principal factor was named *low seed weight* at Ellerslie and *high yield* at Parkland because of the inconsistency in factor loadings between the two locations; 1000-kernel weight carrying maximum negative loading at Ellerslie and yield per plant maximum positive loading at Parkland. *Low seed weight* explained 12.421% and *high yield* 13.115% of the variability in the data at the respective locations. The contribution of yield and its components towards *low seed weight* at Ellerslie was expectedly low except number of spikelets per spike. On the other hand the contribution of yield components towards *high yield* at Parkland was definitely positive. *Low seed weight* was associated with earliness, as reflected by the factor loadings for heading data at the two locations.

Combining ability analysis

The results of the general combining ability analysis are presented in Table 63. For onset-of-heading Marquis was the highest

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 64. Onset-of-heading

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.4433 0.3217	-0.9317 -0.6616	-0.0733 0.6616	-1.1817 -0.9200	2.0733 2.3117	4.2302 5.2404	-0.1713 -0.2584
Chinook	Reciprocal effects	-0.4583 -0.1667	-	-0.8566 -0.3617	-0.8733 -0.9617	-0.1066 -0.1617	1.2483 1.5534	1.4898 2.3096	-0.1058 -0.2239
Khush-hal		0.5417 0.3333	-0.2917 -0.5417	-	0.2933 0.4717	0.5183 0.0217	-0.5433 -0.6300	0.2267 0.2935	0.3626 -0.0689
Ciano		0.3333 0.5000	0.1250 0.2500	0.4167 -0.5000	-	0.5433 -0.3700	-1.6100 -2.3216	2.5235 5.2867	0.1134 0.2494
Inia		0.1667 -0.0417	-0.2500 -0.1250	0.0833 0.8750	-0.3750 0.1250	-	-1.1683 -0.9133	1.2965 0.7308	0.4859 0.0782

TABLE 65. Final heading

Marquis		-	0.4517 0.9417	-0.6816 -1.4000	-0.2400 -0.5167	-0.8233 -0.9250	2.2816 2.1917	5.1591 4.6342	-0.1169 -0.4233
Chinook		-1.0417** -0.5833	-	-0.9817 -1.4833	-0.4983 -1.3500	0.8350 -1.2583	1.4983 2.2334	2.1983 4.8185	-0.0489 -0.1277
Khush-hal	Reciprocal effects	0.5000 0.1250	-0.3333 -0.0833	-	0.3683 1.0167	-0.0483 0.8167	-0.2433 -0.5500	0.0124 0.1332	0.3592 0.9634
Ciano		0.6667* 0.5000	0.7083* 0.2917	0.7500** -0.3750	-	0.1433 0.4500	-2.0183 -2.2250	4.0268 4.7811	0.0303 0.6177
Inia		1.0833** 0.2500	-0.4583 0.0417	-0.2500 0.2500	-0.2500 0.0417	-	-1.5183 -1.6500	2.2585 2.5532	0.3491 0.6795

First reading under each column refers to Ullerslie and the second to Parkland.
* Significant at 5% level
**Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 66. Heading-span

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	-0.0600	0.2867	-0.1300	0.3700	0.1967	-0.0175	-0.1405
			0.6200	-0.6883	-1.1467	-0.0050	-0.1033	-0.1874	-0.4982
Chinook		-0.6550	-	-0.2217	-0.2783	0.8200	0.3717	0.0819	-0.1304
		-0.4167		-1.1217	-0.3717	-1.1467	0.6633	0.3419	-0.3700
Khush-hal	Reciprocal effects	-0.0417	-0.0417	-	0.0200	-0.5217	0.2550	0.0088	-0.0968
		-0.1250	0.4583		0.5283	0.7950	0.0967	-0.1887	0.0821
Ciano		0.3333	0.5833	0.2917	-	-0.3550	-0.4533	0.1493	-0.1089
		0.0	0.0417	0.1250		0.8367	0.0967	-0.1887	0.0822
Inia		0.9167**	-0.2083	-0.3333	0.1250	-	-0.3700	0.0807	0.2620
		0.2917	0.2500	-0.6250	-0.0883		-0.7533	0.3694	0.3871

TABLE 67. Plant height

Marquis		-	-0.9476	0.7593	2.0884	-3.1655	14.0397	195.9310	-2.9557
			-0.2017	2.1257	2.3297	-4.4209	12.5270	155.3739	-3.8799
Chinook		-0.8675	-	-1.0681	0.9945	5.5803	9.8603	96.0433	-2.6564
		1.6562		0.3258	0.1680	2.0856	12.5012	154.7285	3.8664
Khush-hal	Reciprocal effects	2.7857	2.4108	-	0.4511	0.6493	-8.6035	72.8374	-2.3832
		2.7450	1.8100		2.1056	-0.9884	-8.7700	75.3602	-2.3383
Ciano		5.4176**	0.8667	-0.8083	-	-2.4269	-6.1142	36.2005	-1.1045
		5.5917**	2.7682	0.1045		-1.6792	-7.7160	57.9532	-0.5836
Inia		4.6572**	4.8180**	2.4962	0.4758	-	-9.1824	83.1345	12.8684
		3.6565*	3.6762*	-0.8220	-0.1612		-8.5442	71.4512	5.3504

First reading under each column refers to Ellerslie and the second to Parkland.
* Significant at 5% level
**Significant at 1% level

in GCA and Ciano was the lowest. Marquis at Ellerslie and Chinook at Parkland ranked first for final heading while Ciano at both locations ranked last. For heading-span, Chinook showed the highest GCA and Inia the lowest at both locations. Marquis was the best combiner for plant height at both locations, while Inia at Ellerslie and Khush-hal at Parkland were the poorest. Chinook showed the highest GCA for number of tillers per plant at both locations and Inia was the lowest. Interpretations of GCA's for number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight may be made in the same way. For yield per plant, Inia at Ellerslie and Marquis at Parkland had the highest GCA while Chinook at Ellerslie and Ciano at Parkland were the poorest.

The estimates of specific combining abilities, reciprocal effects and variances for general and specific combining abilities for onset-of-heading, final heading and heading-span are presented in Tables 64, 65 and 66. For onset-of-heading, cross (CxI) at Ellerslie and (MxC) at Parkland had the highest SCA while cross (MxI) at Ellerslie and (CHxC) at Parkland scored lowest. The best hybrid (CxI) at Ellerslie had parents with the lowest GCA's at both locations while the worst (MxI) and (CHxC) had one parent Marquis and Chinook which showed the highest GCA's at both locations. The variances for GCA were greater than those for SCA in all cases and the reciprocal effects were not significant. Interpretations for final heading (Table 65) and heading-span (Table 66) may be made in the same way.

For plant height (Table 67), hybrid (CHxI) at both locations

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from 6-fold backcross diallel set at two locations.

TABLE 68. Number of tillers per plant

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	-0.2510 -0.1161	-0.7515 -0.5486	0.5171 -0.6927	0.2983 -1.0161	0.0554 0.7212	-0.1926 0.3487	-0.4891 -0.4286
Chinook	Reciprocal effects	-0.8792 0.1237	-	-0.0109 -0.7988	1.0864 0.2752	-0.1939 0.6594	0.5642 0.7512	0.1227 0.3928	-0.4681 -0.4241
Khush-hal		-0.1787 -0.6792	-0.6125 -0.4780	-	0.1419 0.7439	0.6200 0.4993	0.3819 0.3598	-0.0498 -0.0448	-0.3008 -0.1156
Ciano		0.5208 1.3028*	-0.4260 0.7470	0.3883 0.2823	-	-0.6341 -0.3619	-0.0788 -0.7265	-0.1894 0.3563	0.0001 -0.0590
Inia		-0.1833 -0.0542	0.3333 0.5690	0.4685 -0.2125	-0.0167 0.0857	-	-0.9226 -1.1017	0.6556 1.0423	-0.1848 0.1873

TABLE 69. Number of spikelets per spike

Marquis		-	0.0734 0.5629	0.0484 0.1757	0.2201 -0.0347	-0.1514 -0.0883	0.7318 0.5099	0.5031 0.2252	-0.0810 -0.0870
Chinook	Reciprocal effects	-0.1043 0.2835	-	-0.0157 -0.0718	0.5060 -0.0863	-0.3085 0.1980	0.1207 0.3313	-0.0178 0.0750	-0.0792 0.0186
Khush-hal		0.2930 0.2293	0.2042 0.0835	-	0.1958 0.3633	0.3165 0.0295	-0.4789 -0.2941	0.1969 0.0517	-0.0801 -0.0750
Ciano		0.5625* 0.4038	-0.0867 0.4050	0.0905 0.4162	-	-0.1921 0.1660	-0.2321 -0.4894	0.0215 0.2047	0.0346 -0.0402
Inia		-0.1140 0.1040	0.3238 0.0657	0.1035 0.0598	-0.4457 -0.2070	-	-0.1415 -0.0577	-0.0124 -0.0315	0.0041 -0.0595

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability ability from selfed backcross diallel set at two locations.

TABLE 70. Number of seeds per spike

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	-0.7567 1.1823	0.5266 0.3948	1.6680 1.0759	-1.1312 -0.8422	3.7367 1.8352	13.2888 2.9362	-1.6658 -1.0793
Chinook		-0.6193 0.3758	-	-1.5155 -0.9669	1.7828 0.2750	0.5295 1.0215	-2.1008 -1.0605	4.1253 0.7357	-1.4949 -0.6134
Khush-hal	Reciprocal effects	2.2508* 0.4473	0.6265 1.2037	-	-0.6317 -0.6815	1.1138 -0.3786	-1.2477 0.4308	0.8823 -0.2461	-0.8277 -0.7157
Ciano		3.6903** 1.9765	1.2765 2.0132	0.1728 1.6680	-	0.4189 1.2470	-1.6029 -1.8508	1.8950 2.7759	-0.4341 -0.5141
Inia		-0.1847 0.1222	1.2072 -0.5362	-1.7647 -0.0292	-1.2285 -1.0437	-	1.3047 0.6653	1.0280 0.0109	-0.6937 -0.0279

TABLE 71. Weight of seeds per spike

Marquis		-	0.0198 0.0547	0.0027 0.0141	0.0572 0.0700	-0.0088 0.0494	0.0230 -0.0314	-0.0013 -0.0005	-0.0045 -0.0039
Chinook		0.0158 0.0358	-	-0.0387 -0.0251	0.0596 0.0011	-0.0314 -0.0083	-0.1290 -0.0845	0.0148 0.0056	-0.0044 -0.0030
Khush-hal	Reciprocal effects	0.0618 0.0115	0.0010 0.0585	-	-0.0354 -0.0536	0.0368 0.0111	-0.0362 0.0607	-0.0005 0.0021	-0.0040 -0.0037
Ciano		0.0838 0.0322	0.0058 0.0008	-0.0500 0.0683	-	-0.0179 0.0659	-0.0017 -0.0282	-0.0018 -0.0008	-0.0018 -0.0013
Inia		-0.0382 -0.0605	0.0082 -0.0293	-0.0368 -0.0732	-0.0763 -0.0942	-	0.1439 0.0834	0.0189 0.0054	-0.0036 -0.0016

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 72. 1000-kernel weight

♀ Parent		Specific combining ability					GCA	Variance of GCA	Variance of SCA
		Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis		-	0.1205 0.3031	-0.4528 0.0634	-0.2338 0.5471	0.7582 1.7552	-2.3425 -2.0504	5.0186 3.8294	-1.1713 -0.9369
Chinook		0.6497 6.4662	-	0.4032 0.0455	-0.1392 -0.2633	-1.1356 -0.8131	-1.1454 -1.0151	0.8434 0.6557	-1.1665 -0.9063
Khush-hal	Reciprocal effects	-0.2560 -0.0027	-0.3190 0.5133	-	-0.3410 0.5745	0.0372 0.2047	0.2448 0.9964	-0.4096 0.6180	-1.0488 -0.9325
Ciano		-0.9073 -0.8827	-0.9833 -0.2765	-1.1687 0.1982	-	-0.8553 0.5392	1.4072 0.9224	1.5116 0.4760	-1.1070 -0.7040
Inia		-1.5043 -1.1452	-0.5807 -0.1232	0.6037 -1.6265	-0.5812 -1.2087	-	1.8379 1.1468	2.9294 0.9405	-0.3055 0.4212

TABLE 73. Yield per plant

Marquis		-	-0.7261 0.5455	-0.3666 0.4427	0.7549 0.1542	0.5342 0.1742	-0.0471 -0.5386	-0.2104 0.0529	-0.5317 -0.5930
Chinook		-0.7872 0.9510	-	0.0090 -1.0145	2.2304 0.3140	-0.7179 0.4450	-0.8473 0.0681	0.5052 -0.2316	-0.3559 -0.4939
Khush-hal	Reciprocal effects	0.4678 0.0278	-0.4883 0.3863	-	0.2590 0.4008	0.3710 0.7432	-0.7653 0.3231	0.3731 -0.1328	-0.4868 -0.1846
Ciano		-0.3572 0.7125	-0.6105 0.7283	0.1253 1.4295*	-	-1.7015 -0.5442	0.6451 -0.2341	0.2034 -0.1824	1.3389 -0.4987
Inia		-0.1232 0.2003	-0.2025 0.5000	-0.0010 -0.4568	0.0565 -0.1675	-	1.0147 0.3815	0.8169 -0.0917	0.7462 -0.2341

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

ranked highest while (MxI) ranked lowest. One parent of (CHxI), Chinook, showed the second highest GCA and the other, Inia, the lowest GCA at both locations. Similarly one parent of (MxI), Marquis, showed the highest GCA and other parent, Inia, the lowest GCA at both locations. The variances for GCA were greater in all the cases than those for SCA, and the reciprocal effects were non-significant, except for (CxM), (IxM) and (IxCH) at both locations. These effects may be attributed to the female parents of the respective crosses, because of the positive sign appended to each effect.

For number of tillers per plant, (CHxC) at Ellerslie and (KxC) at Parkland scored highest for SCA while cross (MxK) at Ellerslie and (MxI) at Parkland scored lowest (Table 68). The highest scoring hybrids at both locations had one parent, Ciano, with the second lowest GCA, while the poorest hybrids had one parent, Marquis, scoring second highest for GCA at both locations. The variances for GCA were greater than those for SCA except for Khush-hal at both locations and for Marquis and Ciano at Ellerslie. The reciprocal effects were generally non-significant except for (CxM) at Parkland. The results of the specific combining ability analysis for number of spikelets per spike (Table 69), number of seeds per spike (Table 70), weight of seeds per spike (Table 71) and 1000-kernel weight (Table 72) may be interpreted in the same way. Respective changes in the relative positions of the parents and hybrids for their GCA's and SCA's may be pointed out accordingly.

For yield per plant (Table 73), (CHxC) at Ellerslie and (KxI) at Parkland ranked highest for SCA while cross (CxI) at Ellerslie

TABLE 74

Analysis of variance of general and specific combining ability and reciprocal effects from selfed backcross diallel set at two locations.

Character	M.S. for GCA	M.S. for SCA	M.S. for Reciprocal effects	Error M.S.
D.F.	4	10	10	48
Onset-of-heading	25.2650**	1.5062**	0.2253	0.2568
	35.9375**	1.0437*	0.3587	0.3877
Final heading	34.6875**	0.0500**	0.8927	0.1753
	44.3750**	3.8562**	0.1934	0.6340
Heading-span	1.4006**	0.4038	0.3882	0.2107
	2.5920**	1.9051	0.1924	0.7428
Plant height	1225.0937**	13.5937**	19.2065**	4.4336
	1306.5469**	13.6375*	16.0161**	5.8198
Number of tillers per plant	3.3135**	0.7684	0.4297	0.7332
	7.3857**	1.3497*	0.6839	0.6427
Number of spikelets per spike	2.1357**	0.2266	0.1581	0.1166
	1.7500**	0.2414	0.1404	0.1306
Number of seeds per spike	61.4688**	3.6574	5.4534*	2.5252
	21.4844**	2.8805	2.7848	1.6190
Weight of seeds per spike	0.0980**	0.0033	0.0059	0.0068
	0.0469**	0.0095	0.0066	0.0059
1000-kernel weight	30.5469**	1.0941	1.4095	1.7574
	21.0039**	2.0250	1.3617	1.4052
Yield per plant	6.8789**	2.5621**	0.3304	0.7980
	1.4990	0.7430	0.9333	0.8897

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
**Significant at 1% level

and (CHxK) at Parkland ranked lowest. The best hybrid at Ellerslie had one parent (Chinook) with the lowest GCA for that location while the best hybrid (KxI) at Parkland had one parent (Khush-hal) with the second lowest GCA for that location. On the other hand, the poorest ranking hybrid (CxI) at Ellerslie had one parent, Inia, with the highest GCA for that location while the lowest scoring hybrid at Parkland had one parent (Chinook) with the second highest GCA for that location. Variances for GCA were larger than those for SCA except for Marquis at Ellerslie, Chinook, Khush-hal and Inia at Parkland, and Ciano at both locations. Only cross (IxK) at Parkland showed significant reciprocal effect which may be ascribed to Inia.

Analysis of variance of general and specific combining ability (Table 74) yielded significant mean squares for GCA for all characters except for plant height, number of tillers per plant and yield per plant at Parkland. Significance for SCA mean squares for onset-of-heading, final heading and plant height at both locations, and for yield per plant at Ellerslie show a relatively greater importance of SCA over GCA for these characters in the selection procedures of the breeding programmes.

Diallel cross analysis

The assumption of no differences between reciprocal crosses is tested in Table 75. Significance of the c component for plant height, number of seeds per spike and 1000-kernel weight at both locations and heading-span and weight of seeds per spike at Parkland indicates reciprocal

TABLE 75

Mean squares from the analysis of variance of 5 x 5 selfed backcross diallel set for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Fatal heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
a	4	75.7813**	104.0781**	4.3618*	3675.7500**	9.9355	6.4016**	184.4062**	0.2962*	91.6406**	20.6309
		187.8125**	133.2812**	7.7773	3919.7500**	22.1445**	5.2451*	64.4669**	0.1468*	62.9531**	4.5000
b	10	4.5612**	3.1675**	1.2113	40.6000*	2.3090	0.6820	11.0250	0.0099	3.3000	7.6895
		3.1750	11.5562**	5.7149	49.9000	4.0539	0.7270	8.6687	0.0286	6.0937	2.2301
b_1	1	14.8519	6.5209	0.6533	25.4775	2.0285	1.4763	12.0519	0.0001	10.1405	1.2529
		12.1002	41.2552	8.6700	10.2661	5.5196	4.5690*	19.1386	0.0721	10.3402	5.1668
b_2	4	2.5469	2.3125	1.2256	22.5000	1.4173	0.8340	10.5586	0.0095	2.4014	6.3564
		1.1406	5.7969	4.6944	61.6094	5.2782	0.0742	11.3848	0.0482	9.7090	0.3721
b_3	5	4.1375**	3.1625**	1.3086**	59.2000*	3.0828*	0.4086	11.1500	0.0124	2.6750	10.0445
		3.6000	10.2500**	5.9492**	30.6375*	2.7836**	0.4307	4.4373	0.0044	2.3750	3.1320
c	4	0.6323	2.4437	0.8052	124.9227**	1.1638	0.6298	31.4601*	0.0241	6.2645**	0.5412
		0.4510	0.2865	0.6425*	111.7265**	2.3081	0.9578	18.2904**	0.0421**	6.9694*	4.0602
d	6	0.7052	2.8344	1.4042	13.1473	1.3726	0.3740	6.2935	0.0134	2.8714	1.2913
		1.4927	0.7094	0.5201	5.6094	1.8806	0.0632	1.7307	0.0049	2.1623	1.9465
Blocks x *a*	8	0.6094	0.5313	0.6566	35.1494	4.2528	0.6206	21.3906	0.0553	12.6406	3.5356
		1.5469	2.9687	5.7076	26.2500	3.4097	0.0687	11.5391	0.0357	7.3256	5.3936
Blocks x *b*	20	1.1750	0.6219	0.7967	11.6469	1.7096	0.4297	6.4000	0.0207	5.1812	2.6195
		1.5375	2.7594	2.6783	27.2594	2.4264	0.6600	5.3156	0.0241	5.0729	2.7564
Blocks x b_1	2	7.9587	1.2337	3.9429	35.3591	0.8380	0.9345	30.6816	0.0527	1.9096	2.5027
		4.9006	22.6079	9.6837	343.6152	29.1593	0.0720	1.6645	0.0962	31.9250	3.6281
Blocks x b_2	8	1.4365	0.7158	1.3752	11.5615	3.3234	0.5036	6.4000	0.0332	9.9072	5.2374
		1.9155	3.1094	4.2928	27.5938	2.0966	0.8176	10.4960	0.0398	6.9990	3.9131
Blocks x b_3	10	0.4187	0.6062	0.0968	10.7312	0.6729	0.3559	4.7937	0.0095	2.2551	0.7465
		1.0375	1.5125	0.9535	8.1167	0.2590	0.2363	2.0675	0.0065	1.3609	2.0207
Blocks x *c*	8	0.4482	0.7219	0.6130	6.4503	1.0612	0.2022	4.9007	0.0101	0.6612	1.3497
		0.7901	0.5036	0.1562	5.2479	0.9600	0.1437	1.2592	0.0036	1.3100	1.0076
Blocks x *d*	12	0.3979	0.2679	0.3552	6.2170	2.4183	0.2015	2.2132	0.0034	3.5959	1.9556
		0.5323	0.7042	0.5399	3.8175	0.7433	0.1323	2.0795	0.0048	2.7544	1.2823
Error	48	0.7047	0.8299	0.6024	13.3400	2.3025	0.3645	7.6519	0.0204	5.2758	2.3846
		1.1632	1.9045	2.2333	17.5610	1.3319	0.3936	4.8671	0.0178	4.3249	2.6731

* Significant at 5% level
**Significant at 1% level
First reading under each column refers to Kiloralin and second to Parkland. Error D.F. comprises of block interaction with D.F. of *(subgroup)*. Each component has been tested against its own block interaction.

TABLE 76

Analysis of variance of $W_r - V_r$
from selfed backcross diallel set for ten characters at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.
Onset-of-heading	0.6481 3.6665	0.3595 0.5120	0.3829 0.2390
Final heading	0.6143 34.1073	0.1781 1.1282	0.1925 1.2708
Heading-span	1.3027 4.9259	1.7102 0.4529	0.6124 1.3644
Plant height	9647.4543 6449.6875	199.[illegible] [illegible]	55.0016 194.[illegible]
Number of tillers per plant	3.0944 2.6647	0.2674 0.4159	0.8126 0.3661
Number of spikelets per spike	1.0906 0.0002	0.0195 0.0096	0.0485 0.0294
Number of seeds per spike	236.2762 27.1069	9.9644 2.0640	15.9139 6.1681
Weight of seeds per spike	0.0020 0.0014	0.00 0.0001	0.00 0.0001
1000-kernel weight	156.5755 18.6693	1.5762 5.1193	2.7423 5.6779
Yield per plant	13.4404 0.0343	0.2740 0.1468	0.4405 0.8250

First reading under each column refers to Ellerslie and second to Parkland.

TABLE 77

Estimates of second degree statistics from selfed backcross diallel set for ten characters at two locations.

Character	$V_{(r)}$	$V_{(rs)}$	$V_{(r)}$	$V_{(s)}$	$(\bar{W}_{(r)} - \bar{W}_{(s)})^2$
Onset-of-heading	15.0000 15.7002	6.1531 7.4624	2.5312 3.5977	3.2941 4.1244	0.7921 0.6454
Final heading	16.7446 27.1514	7.6016 10.9432	3.4756 4.4463	4.0049 6.3744	0.3481 2.2201
Heading-span	0.5869 3.6111	0.2319 0.9279	0.1462 0.2593	0.3480 1.2118	0.0348 0.4624
Plant Height	486.7744 516.4434	241.1329 257.2312	122.5254 130.6756	126.3232 137.4928	1.3563 0.5476
Number of tillers per plant	1.4343 5.4749	0.6990 1.8630	0.3313 0.7383	0.7159 1.4139	0.1081 0.2944
Number of spikelets per spike	1.2283 0.5749	0.4769 0.3149	0.2136 0.1750	0.3275 0.2965	0.0787 0.2436
Number of seeds per spike	28.9983 12.2.75	12.8658 4.6342	6.2455 2.1465	7.9799 3.5906	0.6427 1.0207
Weight of seeds per spike	0.0384 0.0160	0.0169 0.0115	0.0098 0.0049	0.0115 0.0087	0.0003 0.0038
1000-kernel weight	16.7744 13.2670	7.1279 4.9039	3.0537 2.0977	3.6014 3.1123	0.5408 0.5517
Yield per plant	5.4558 0.6675	1.7342 0.3533	0.6160 0.1502	1.4697 0.5220	0.0668 0.2755

First reading under each column refers to Ellerslie and second to Parkland.

differences for these characters. Significance of the a for all characters except heading-span at Ellerslie, number of tillers per plant at Parkland and yield per plant at both locations indicates substantial differences among the parents. Significance of b for final heading at both locations and onset-of-heading and plant height at Ellerslie shows that dominance is present while b_1 for number of spikelets per spike at Ellerslie shows that dominance is directional. Analysis of $W_r - V_r$ (Table 76) indicates that other assumptions, viz., no non-allelic interaction, no multiple allelism and uncorrelated gene distribution, are valid for all characters at both locations.

After Hayman's (1954a) procedure of replacement of reciprocal crosses by their common means, diallel analysis for genetic components of variation was carried out. Estimates of second degree statistics are given in Table 77 and the genetic components of variation obtained from them are presented in Table 78. Significance of components of variation was tested as in the previous diallel analyses of F_1, F_2 and backcross sets. The proportional values of the estimates of genetic parameters from Table 78 are given in Table 79.

The ratio $(H_1/D_1)^{1/2} < 1$ for onset-of-heading at both locations (Table 79) shows that dominance is partial (see also Figure 61). The estimate of $[H_2 \div 4H_1] = 0.21$ at Ellerslie and 0.24 at Parkland implies some asymmetry in numbers of positive and negative alleles at loci exhibiting dominance at Ellerslie and equal proportion of positive and negative effects at Parkland. The proportion of dominant to recessive genes in the parents is > 1 at both locations indicating thus

TABLE 7H

Estimates of genetic components of variation
from selfed backcross diallel set for ten characters at two locations.

Character	D	F	H_1	H_2	h^2	E
Onset-of-heading	14.7431 ± 0.2183**	5.0792 ± 0.5453**	2.8960 ± 0.5395**	2.5377 ± 0.5347**	3.0042 ± 0.3610**	0.2569 ± 0.0891**
	15.3126 ± 0.1216**	1.0837 ± 0.3037**	1.3386 ± 0.3282**	1.3319 ± 0.2978**	2.3336 ± 0.2010**	0.3876 ± 0.0496**
Final heading	14.7914 ± 0.1955**	3.3169 ± 0.4884**	2.1242 ± 0.5200**	1.7665 ± 0.4789**	1.7824 ± 0.3233**	0.1753 ± 0.0798**
	26.5164 ± 0.5972**	9.7681 ± 1.4668**	7.2254 ± 1.5858**	6.4425 ± 1.4383**	8.3949 ± 0.9711**	0.6350 ± 0.2397**
Heading-span	0.1781 ± 0.1789	-0.0027 ± 0.4468	0.5056 ± 0.4831	0.3859 ± 0.4301	0.0045 ± 0.2958	0.3108 ± 0.0750**
	2.8484 ± 0.3616**	2.6196 ± 0.9034**	2.8158 ± 0.9766**	2.3245 ± 0.8058**	1.3742 ± 0.5981**	0.7428 ± 0.1476**
Plant height	482.3858 ± 5.9180**	-4.1831 ± 14.7833	20.1284 ± 15.9824	18.3242 ± 14.4962	2.5981 ± 9.7670	4.4336 ± 2.4160**
	512.4233 ± 4.8412**	1.0942 ± 12.0934	28.4779 ± 13.0743	15.6281 ± 11.8565	-1.5344 ± 8.0062	5.8199 ± 1.9764**
Number of tillers per plant	0.7006 ± 0.1906**	-0.4973 ± 0.4761	-0.0492 ± 0.5256	0.0710 ± 0.4767	-0.6369 ± 0.3218	0.7337 ± 0.0795**
	4.6319 ± 0.2063**	2.6062 ± 0.5145**	2.0868 ± 0.5562**	1.4165 ± 0.5045**	0.7661 ± 0.3406	0.6429 ± 0.0841**
Number of spikelets per spike	1.1068 ± 0.0401**	0.3453 ± 0.1001*	0.3072 ± 0.1632	0.2130 ± 0.1472	0.2372 ± 0.0994**	0.1215 ± 0.0245**
	0.4444 ± 0.0434**	-0.2666 ± 0.1084	0.1616 ± 0.1172	0.2248 ± 0.1063	0.6911 ± 0.0718**	0.1305 ± 0.0177**
Number of seeds per spike	26.6696 ± 0.7975**	3.4994 ± 1.9922**	2.8758 ± 2.1538	2.2802 ± 1.9535	0.9525 ± 1.3189	2.5286 ± 0.3256**
	20.6286 ± 0.7635**	3.9757 ± 1.9072**	3.8441 ± 2.0619	2.5367 ± 1.8702	3.0465 ± 1.2626**	1.6169 ± 0.3117**
Weight of seeds per spike	0.0316 ± 0.0009**	-0.0017 ± 0.0023	-0.0092 ± 0.0025**	-0.0070 ± 0.0022**	-0.0043 ± 0.0015**	0.0068 ± 0.0004**
	0.0301 ± 0.0025**	0.0190 ± 0.0062**	0.0133 ± 0.0067**	0.0072 ± 0.0061	0.0116 ± 0.0041**	0.0059 ± 0.0010**
1000-kernel weight	15.0175 ± 0.3606**	2.9288 ± 0.9008**	-1.6999 ± 0.9739	-1.3233 ± 0.8833	1.0390 ± 0.5964	1.7569 ± 0.1472**
	11.7616 ± 0.7518**	5.0319 ± 1.8779**	2.3466 ± 2.0302	1.2478 ± 1.8414	1.3076 ± 1.2432	1.4354 ± 0.3069**
Yield per plant	8.0583 ± 1.1859**	3.0180 ± 2.9624	4.3245 ± 3.2027	3.5319 ± 2.9049	-0.2431 ± 1.9612	0.7975 ± 0.4841**
	-0.6021 ± 0.1412	-0.7056 ± 0.3527	-0.7503 ± 0.3814	-0.2918 ± 0.3459	0.5329 ± 0.2335	0.8896 ± 0.0476**

First reading under each column refers to Ellerslie and second to Parkland.
* Significant at 5% level
**Significant at 1% level

TABLE 79

Proportional values of the estimates of genetic parameters from selfed backcross diallel set for ten characters at two locations.

Character	$[H_1/D]^{1/2}$	$[H_2/4H_1]$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}\right]$	h^2/H_2	r_{Y_r, W_r+V_r}	Heritability
Onset-of-heading	0.4432*	0.2119*	2.2715*	1.1839*	0.9161	1.0850
	0.2957*	0.2487*	1.2719*	1.7521*	0.6870	0.8045
Final heading	0.3557*	0.2079*	1.7089*	0.7248*	0.7816	1.0301
	0.5220*	0.2229*	2.0905*	1.3030*	0.9245	1.0001
Heading-span	1.1562	0.1909	0.9939	0.0116	-0.0581	0.2186
	0.9908*	0.2064*	2.7079*	0.5912*	0.7279	0.4752
Plant height	0.2043	0.2276	0.9584	0.1418	-0.4065	0.9198
	0.2185	0.1596	1.0099	-0.0982	-0.6697	0.9165
Number of tillers per plant	0.3488	-0.2083	0.0013	-0.5189	-0.7486	0.1735
	0.6572*	0.1697*	2.5834*	0.5408	0.6240	0.7228
Number of spikelets per spike	0.5268	0.1733	2.0258	1.1137	-0.8852	0.7355
	0.6031	0.3477	0.3357	3.9638	-0.0175	0.3186
Number of seeds per spike	0.3298	0.1979	1.5011	0.4177	-0.6535	0.7359
	0.6020	0.1651	1.9039	1.2000	-0.5060	0.6257
Weight of seeds per spike	0.5392	0.1904	0.6546	0.6502	0.9431	0.6159
	0.6049*	0.1357	2.8052*	1.6045	-0.2946	0.6270
1000-kernel weight	0.3557	0.1741	1.7554	-0.7852	0.3482	0.8722
	0.4467	0.1329	2.8281	1.0479	-0.8856	0.8002
Yield per plant	0.9635	0.2042	2.0130	-0.0688	0.3272	0.5088
	18.9020	0.0972	-0.7970	-1.8262	-0.5945	-0.0005

First reading under each column refers to Ellerslie and second to Parkland.
*Proportional values involving genetic components of variation significantly different from zero ($P \leq 0.05$)

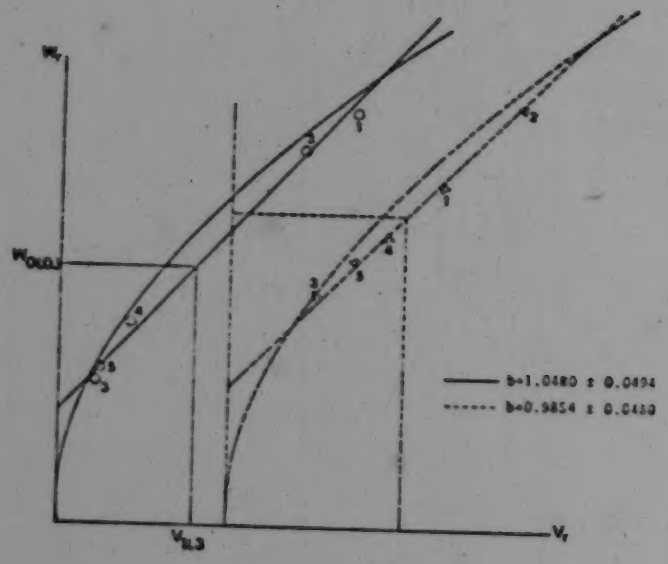

Figure 61. W_r, V_r graph for onset-of-heading from selfed backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

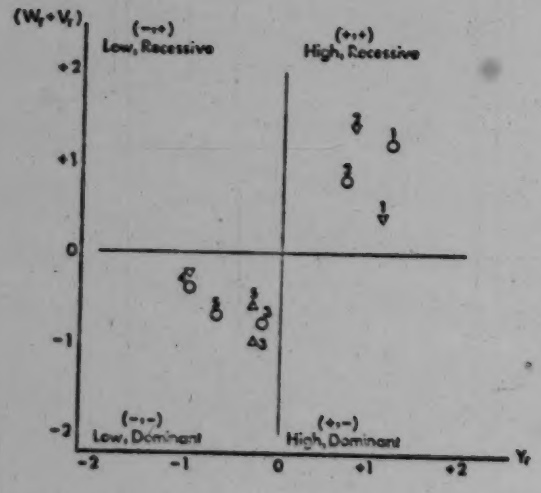

Figure 62. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for onset-of-heading from selfed backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

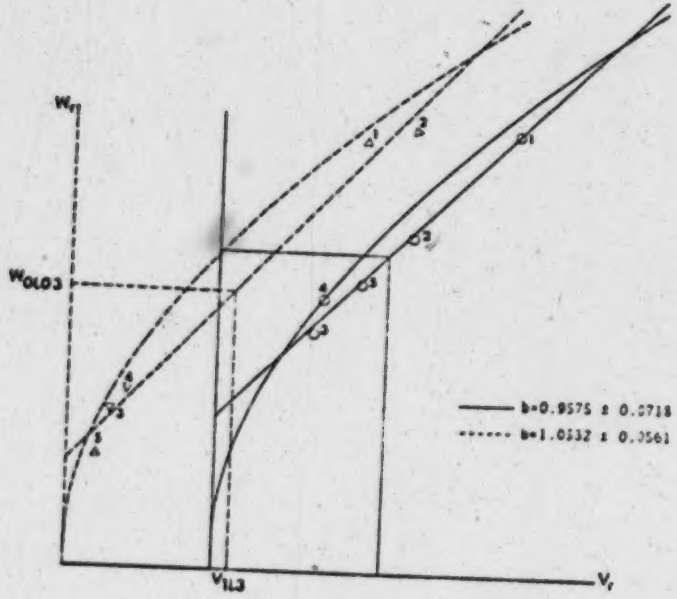

Figure 63. W_r, V_r graph for final heading from selfed backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

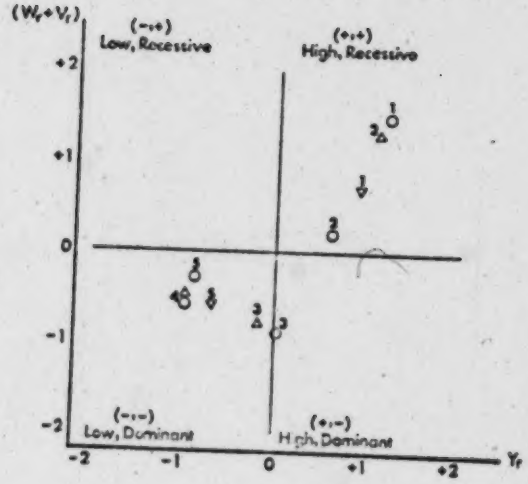

Figure 64. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from selfed backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

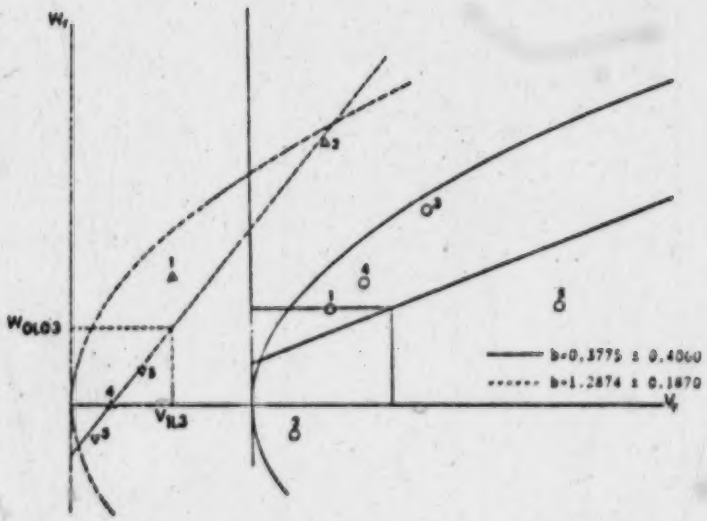

Figure 65. W_r, V_r graph for heading-span from selfed backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

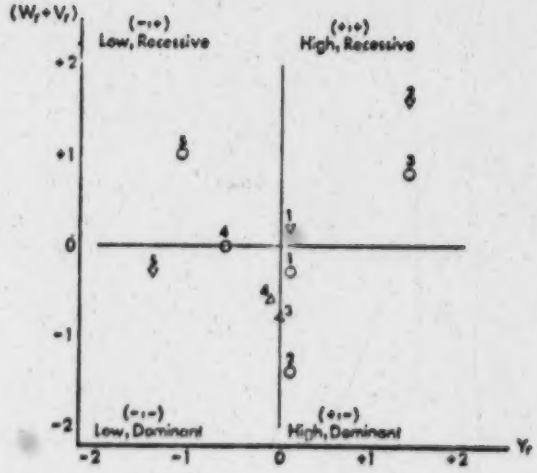

Figure 66. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from selfed backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

a preponderance of dominant genes. $[h^2/H_2] > 1$ at both locations suggests that at least two groups of genes exhibiting dominance contribute to the control of onset-of-heading. The coefficients of correlation between parental order of dominance and parental measurements (0.916 at Ellerslie and 0.687 at Parkland) indicate that earliness is dominant over lateness. Figure 61 shows that Marquis at Ellerslie and Chinook at Parkland are the most recessive parents while Khush-hal at both locations is the most dominant. Figure 62 places Marquis and Chinook in the (+,+) quadrant, indicating that lateness of these parents is associated with recessive genes. Khush-hal, Ciano and Inia occupy the (-,-) quadrant at both locations, suggesting that these parents are early maturing dominants.

The interpretations from Tables 78 and 79 for final heading (Figures 63, 64) and for heading-span (Figures 65, 66) may be made in the similar fashion. The changes in the relative position of the parents with respect to their order of dominance at the two locations could be attributed to environmental effects.

In case of plant height, the ratio of $[H_1/D]^{1/2} < 1$ at both locations indicates that the character is inherited as a partially dominant trait. Since all other components of variation, except D and E are non-significant at both locations (Table 78), the interpretation of proportional values of genetic parameters is meaningless. Figure 67 classifies Ciano at Ellerslie and Khush-hal at Parkland as the most recessive parents and Chinook as the most dominant at both locations. Figure 68 indicates that the most dominant parent (Chinook) at both

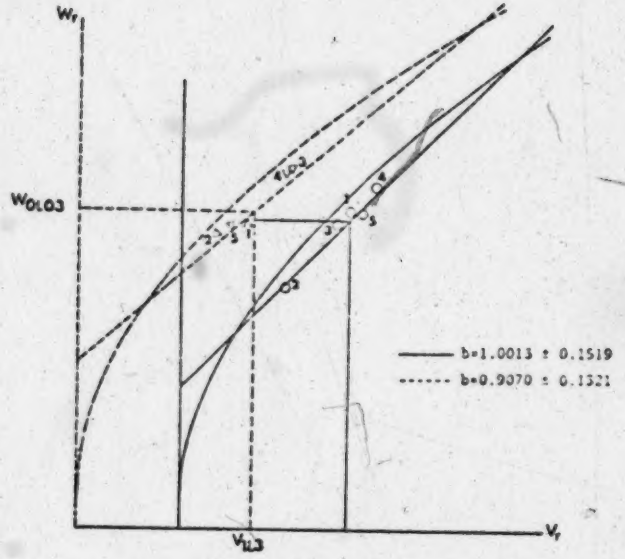

Figure 67. W_r, V_r graph for plant height from selfed backcross diallel set.
—— o = W_r, V_r intercepts at Ellerslie
--- Δ = W_r, V_r intercepts at Parkland

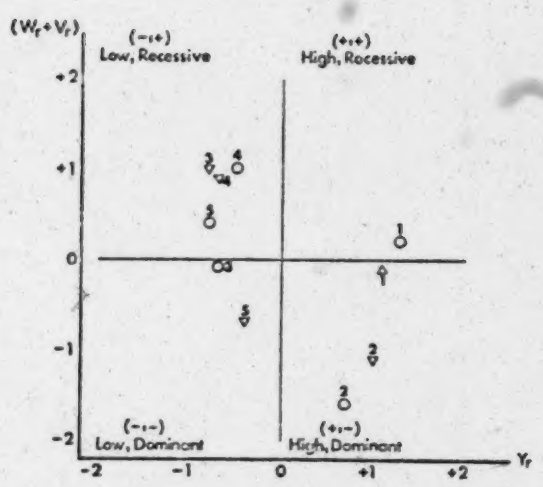

Figure 68. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from selfed backcross diallel set.
o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie
Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

locations, contributes to tallness, while the most recessives (Ciano and Khush-hal) contribute to shortness; i.e. the order of dominance of the parents is negatively correlated with their measurements. However, as shown in Table 79, the respective coefficients of correlation do not reach the 5% level of significance. The order of dominance of parents seems to differ at the two locations (Figure 68). The most recessive parent at Parkland (Khush-hal; -,+ quadrant) possesses an excess of dominant genes (-,- quadrant) at Ellerslie, while Inia with an excess of recessive genes at Ellerslie (-,+ quadrant), appears to have a preponderance of dominants at Parkland (-,- quadrant). Marquis, recessive at Ellerslie becomes dominant at Parkland. The ranking order of Ciano and Chinook remained unchanged. The coefficient of heritability was very high (91%) at both locations.

For number of tillers per plant, only the D and E components of variation were significant at Ellerslie, while all components except h^2 were significant at Parkland. Consequently, the proportional values of the estimates of parameters for Ellerslie data are not discussed. However, the mean degree of dominance may be given, since $(H_1 \div D)^{1/2} < 1$ for both locations indicating that tillering capacity is inherited as partially dominant. The ratio $[H_2 \div 4H_1] = 0.169$ at Parkland suggests asymmetry of positive and negative alleles at loci exhibiting dominance. The proportion of dominant to recessive genes in the parents is 2.58 indicating a preponderance of dominants. Since $[h^2/H_2] = 0.54$, it may be assumed that at least one group of genes exhibit dominance and control the inheritance of tiller number. The correlation coefficient between

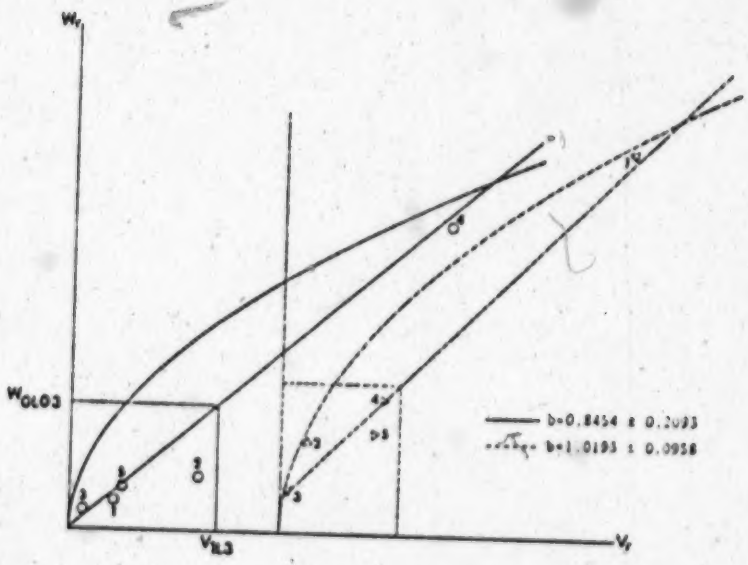

Figure 69. W_r, V_r graph for number of tillers per plant from selfed backcross diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

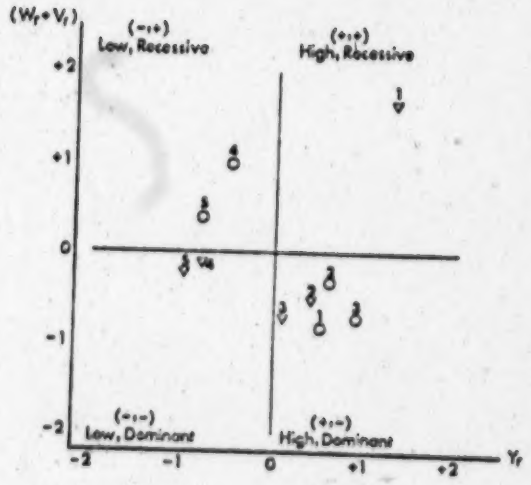

Figure 70. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from selfed backcross diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

parental order of dominance and parental mesurements is -0.748 at Ellerslie and 0.624 at Parkland. The significant negative correlation at Ellerslie indicates that the high tillering capacity is dominant over low tillering capacity while positive correlation at Parkland concludes that lower tiller number is dominant over higher. Figure 69 classifies Ciano and Khush-hal at Ellerslie as the most recessive and the most dominant parents, respectively. At Parkland, Marquis and Khush-hal are the most recessive and the most dominant parents, respectively. Figure 70 shows changes in the dominance ranking order of the parents between the two locations. Marquis, the most recessive parent at Parkland, (+,+ quadrant) appears to contain an excess of dominant genes at Ellerslie (+,- quadrant) while Ciano and Inia, recessive parents at Ellerslie (-,+ quadrant) appear as dominant at Parkland (-,- quadrant). Ranking order of Khush-hal and Chincok remain unchanged. The heritability estimates of 17.35% at Ellerslie and 72.28% at Parkland show that the character is highly unstable. This unstability may be due to non-significance of genetic components of variation at Ellerslie and significance of environmental components of variation at both locations.

The results of diallel cross analysis from Tables 78 and 79 for number of spikelets per spike (Figures 71, 72), number of seeds per spike (Figures 73, 74), weight of seeds per spike (Figures 75, 76) and 1000-kernel weight (Figures 77, 78) may be interpreted in the same way as number of tillers per plant. Respective changes in the ranking order of parents for order of dominance and significance or non-significance

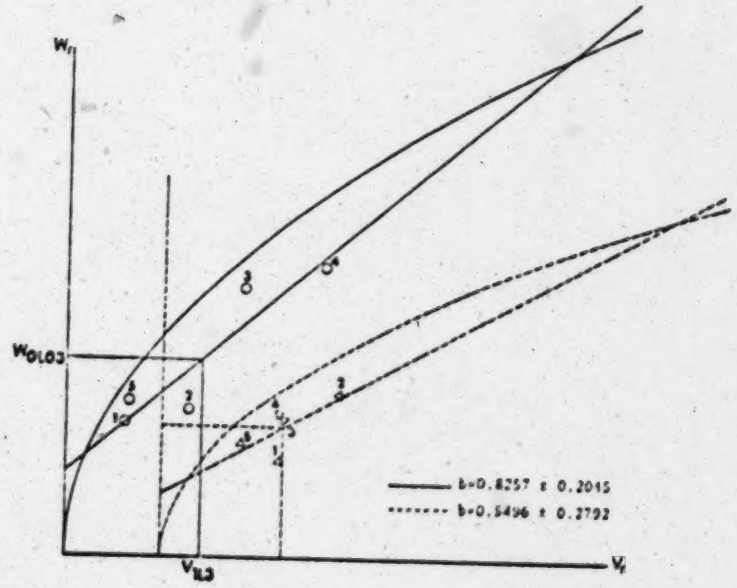

Figure 71. W_r, V_r graph for number of spikelets per spike from selfed backcross diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

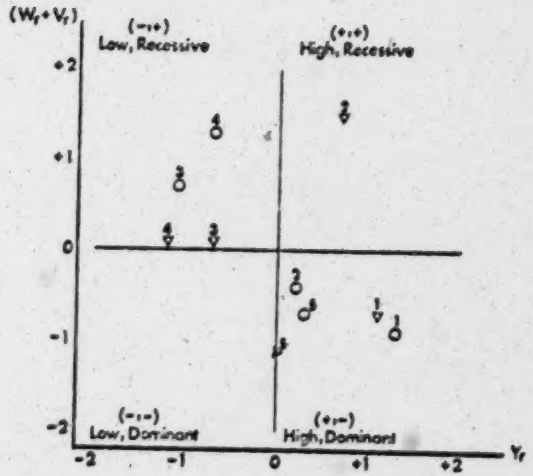

Figure 72. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from selfed backcross diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

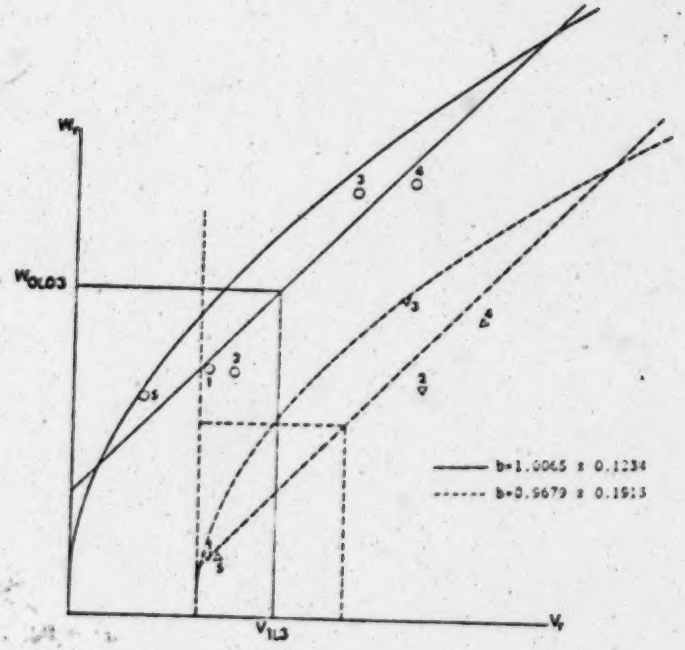

Figure 73. W_r, V_r graph for number of seeds per spike from selfed backcross diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

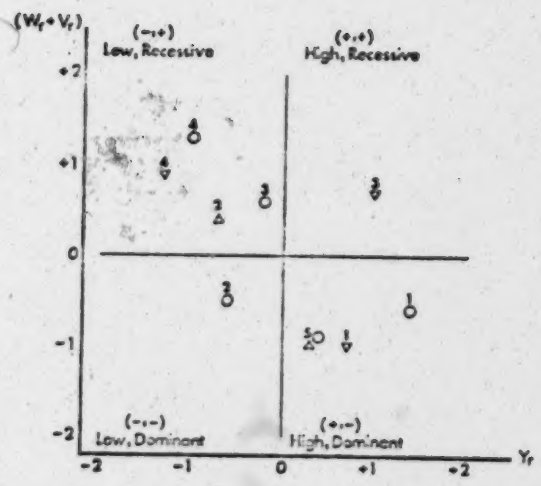

Figure 74. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of seeds per spike from selfed backcross diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

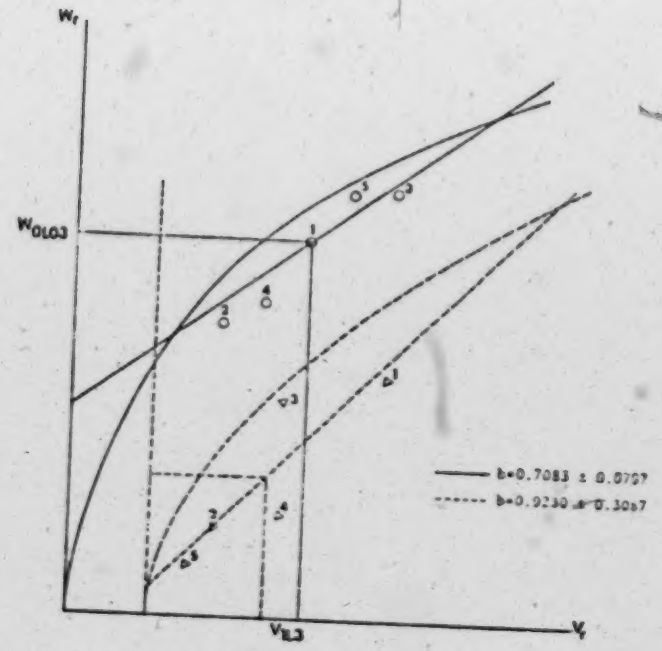

Figure 75. W_r, V_r graph for weight of seeds per spike from selfed backcross diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

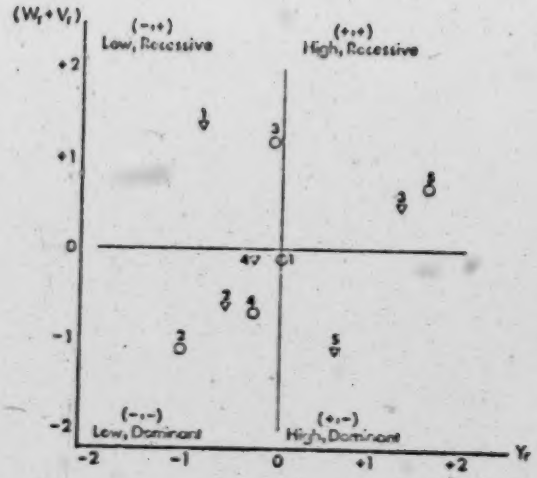

Figure 76. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from selfed backcross diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

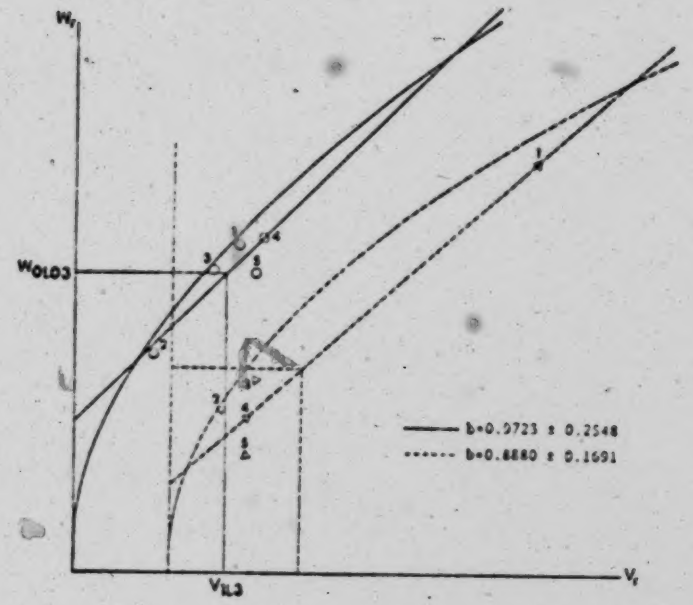

Figure 77. W_p, V_p graph for 1000-kernel weight from selfed backcross diallel set.

—— o = W_p, V_p intercepts at Ellerslie

--- Δ = W_p, V_p intercepts at Parkland

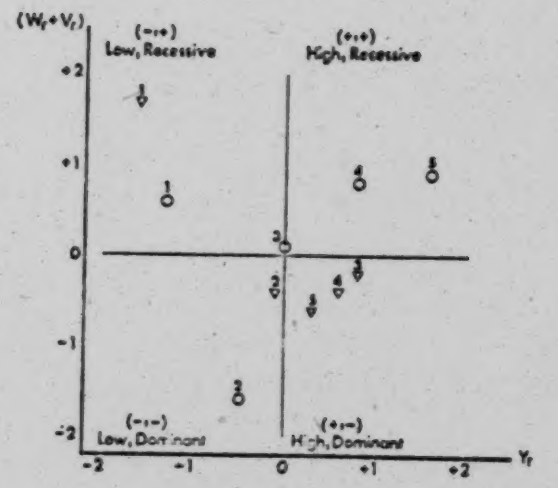

Figure 78. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for 1000-kernel weight from selfed backcross diallel set.

o = Y_p, $[W_p + V_p]$ intercepts at Ellerslie

Δ = Y_p, $[W_p + V_p]$ intercepts at Parkland

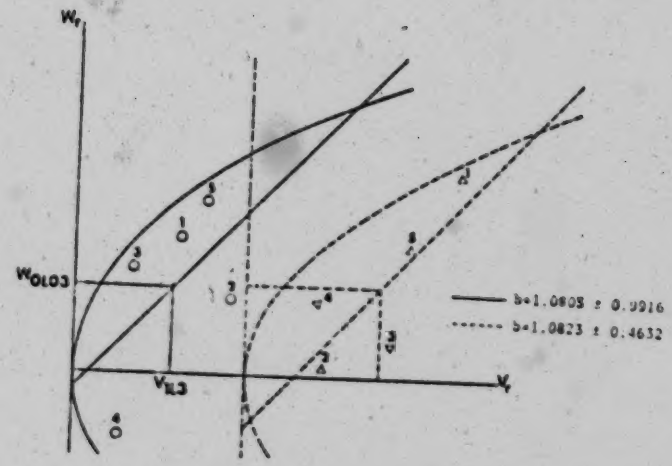

Figure 79. W_r, V_r graph for yield per plant from selfed backcross diallel set.

—— o = W_r, V_r intercepts at Ellerslie

--- Δ = W_r, V_r intercepts at Parkland

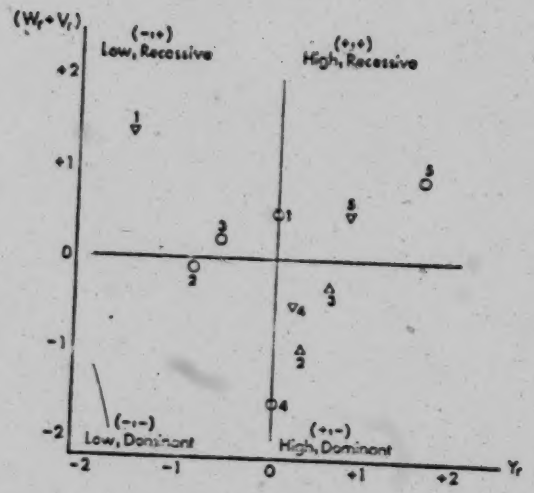

Figure 80. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from selfed backcross diallel set.

o = Y_r, $[W_r + V_r]$ intercepts at Ellerslie

Δ = Y_r, $[W_r + V_r]$ intercepts at Parkland

of genetic components of variation over the two locations may be interpreted accordingly.

In case of yield per plant, all the components of variation except D and E at Ellerslie and E at Parkland were non-significant. The proportional values of the genetic parameters given in Table 79 therefore do not carry valid conclusions. The ratio $[H_1 \div D]^{1/2} > 1$ at Parkland and $\simeq 1$ at Ellerslie suggests over-dominance and nearly complete dominance. The W_r, V_r graph (Figure 79) shows over-dominance at both locations (the regression line intersects the limiting parabola below the origin). The correlation coefficient of 0.327 at Ellerslie and -0.594 at Parkland suggests that low yielding capacity is dominant over high yield at Ellerslie and vice versa at Parkland. Figure 79 categorizes Inia and Ciano as the most recessive and dominant parents, respectively, at Ellerslie, while Marquis and Chinook as the most recessive and dominant parents, respectively, at Parkland. Figure 80 suggests that the highly recessive parent at Ellerslie is high yielding (+,+ quadrant), while the highly recessive parent at Parkland is low yielding (-,+ quadrant). Figure 80 also reveals changes in the ranking of parents with respect to their order of dominance at both locations. Khush-hal, recessive low-yielding at Ellerslie, appears to be dominant high-yielding at Parkland. Marquis, the most recessive parent at Parkland, appears comparatively less recessive at Ellerslie. Inia, Chinook and Ciano remained unchanged. Heritability of 51% at Ellerslie and -0.0005 $\simeq$ 0% at Parkland suggests, respectively, high and non-heritable nature of yield. This reflects the inter-location environmental effect on the inheritance of yield.

GENOTYPE-ENVIRONMENT INTERACTION

This section of the experimental results deals with the comparison of the estimates of factor loadings, general combining abilities and genetic components of variation obtained from the analyses of four diallel sets considered over two locations.

In order to assess the stability of five principal factors with respect to their loadings on different characters, the varimax rotated factor matrices of F_1, F_2, backcross and selfed backcross diallel sets were factorially analysed for two locations. The results of analysis of variance are given in Table 80. Significance of mean squares for principal factors (F) and Characters (C) (upper part of Table 80) suggests that the number of factors required to explain the variability in the data varies with the number and the degree of expression of the characters under study. This is also indicated by significant F x C interaction, which implies that the differences between the contributions of different characters to factor loadings vary with the number of principal components. Significant inter-location effects (L) indicate differences in scores on the characters related to different principal components at different locations. Significance of the second order interaction, L x F x C, may be considered as interactions of the L x F with C, L x C with F, or of F x C with L. Since L x C is not significant, indicating that characters do not vary with locations, the L x F x C interaction may be interpreted in the light of L x F and F x C interactions alone. In the first case, L x F x C indicates that after pooling the sum of squares

TABLE 80

Factorial analysis of variance of factor loadings of varimax rotated factor matrices of F_1, F_2, backcross and selfed backcross diallel sets over two locations.

Source of variation	D.F.	Sum of squares	Mean squares	F ratio
Locations (L)	1	0.23868	0.23868	5.15589*
Principal factors (F)	4	2.73528	0.68382	14.77165**
L x F	4	2.39790	0.59947	12.94968**
Generations (G)	3	0.07528	0.02509	0.54210
L x G	3	0.08975	0.02991	0.64629
F x G	12	0.54642	0.04503	0.97284
L x F x G	12	0.19273	0.01606	0.34695
Characters (C)	9	1.80613	0.20068	4.33507**
L x C	9	0.76141	0.08460	1.82754
F x C	36	22.47183	0.62421	13.48413**
G x C	27	0.54033	0.02001	0.43230
L x F x C	36	7.44184	0.20671	4.46545**
L x G x C	27	0.91759	0.03398	0.73413
F x G x C	108	12.82314	0.11837	2.56482**
Error (L x F x G x C)	108	4.99961	0.04629	-
Locations	1	0.23868	0.23868	1.76766
Principal factors	4	2.73528	0.68382	5.06437**
L x P	4	2.39790	0.59974	4.43972**
Error	390	52.66000	0.13502	-

* Significant at 5% level
**Significant at 1% level

for characters into error sum of squares, the values of factor loadings vary at each location, and in the second case, it shows that the score of factor loadings on each character varies with the number of principal factors, considered independently of locations. Similarly, significant F x G x C interaction may be interpreted considering the interactions of F x G with C, F x C with G and G x C with F. Since F x G and G x C are non-significant, the significance of F x G x C in the presence of a significant F x C means that different factor loadings are carried by characters when averaged over generations.

Generations do not seem to have any effect on the factor loadings nor do they show interaction with principal factors, locations and characters. When the sum of squares for generations are pooled into error (lower part of Table 80), the location effects are not significant but the principal components are, with significant L x F interactions. It follows, therefore, that though on the average there is no significant location effect, the L x F interaction is significant. Thus the contributions of different factor loadings on different characters at different locations are not the same.

The factorial analysis of variance on weighted values for general combining abilities over four generations and two locations is given in Table 81. Individual GCA's were standardized by dividing each value of a particular character by the GCA, averaged over four generations and two locations, for that character. The aim of such standardization preceding *factorial ANOVA* was to normalize the scales for different characters. For example, heading data were taken in number of days,

TABLE 81

Factorial analysis of variance of general combining ability over four generations and two locations.

Source of variation	D.F.	Sum of squares	Mean squares	F ratio
Locations (L)	1	1.71959	1.71959	1.15079
Parents (P)	4	2.54764	0.63691	0.42623
L x P	4	1.11852	0.27963	0.18713
Generations (G)	3	4.27284	1.42428	0.95316
L x G	3	1.78580	0.59526	0.39837
P x G	12	6.27137	0.52261	0.34975
L x P x G	12	3.89558	0.32463	0.21725
Error	360	537.93774	1.49427	-
Locations (L)	1	1.71959	1.71959	1.88320
Parents (P)	4	2.54764	0.63691	0.69752
L x P	4	1.11852	0.27963	0.30624
Generations (G)	3	4.27284	1.42428	1.55981
L x G	3	1.78580	0.59526	0.65191
P x G	12	6.27137	0.52261	0.57234
L x P x G	12	3.89558	0.32463	0.35552
Characters (C)	9	12.89835	1.43315	1.56952
L x C	9	8.39985	0.93331	1.02213
P x C	36	91.33239	2.53701	2.77842***
G x C	27	21.10522	0.78167	0.85606
L x P x C	36	192.26447	5.34067	5.84888***
L x G x C	27	21.24818	0.78696	0.86185
P x G x C	108	92.07365	0.85253	0.93366
Error (L x P x G x C)	108	98.61607	0.91311	-

***Significant at 0.1% level

plant height was measured in centimeters, yield per plant, weight of seeds per spike and 1000-kernel weight were expressed in grams, and number of tillers per plant, number of spikelets per spike and number of seeds per spike were scored as counts. Thus by dividing the GCA of each character by its mean over two locations, the scale differences were removed but the inter-location differences were preserved.

The first part of Table 81 shows a three-way layout analysis of general combining abilities where locations, parents and generations have been treated as main effects. None of the mean squares showed significance. This means that parental lines did not differ in their general combining abilities over the two locations in any generation of the diallel cross. When the characters were introduced as a fourth main effect by analyzing the normalized GCA's in a four-way factorial layout (second part of Table 81), the mean squares for P x C and L x P x C interaction were significant. This suggests that the combining ability values for different characters vary with the number of parents and locations.

It is interesting to note that after introducing characters as separate effects, the mean squares, either for generations or any of the interactions involving generations, were not significant. This indicates that generations do not affect GCA's for any characters in question. The significance of P x C and L x P x C interactions on the other hand provides the possibility for comparing which of the parental lines for their relative adaptability is more

TABLE 82

Analysis of variance of Parkland GCAs' regression upon Ellerslie GCAs' regression for each of the parental lines

Parent	Source of variation	D.F.	Sum of squares	Mean squares	Regression coefficient
Marquis	Due to regression	1	157.5731	157.5731***	
	Due to error	8	1.8675	0.2334	b = 0.9416
Chinook	Due to regression	1	138.6222	138.6222***	
	Due to error	8	1.3375	0.1671	b = 1.1118
Khush-hal	Due to regression	1	62.7426	62.7426***	
	Due to error	8	4.2024	0.5253	b = 1.0769
Ciano	Due to regression	1	60.1872	60.1872***	
	Due to error	8	1.0378	0.1297	b = 1.1163
Inia	Due to regression	1	75.7396	75.7396***	
	Due to error	8	0.4692	0.0586	b = 0.8821

***Significant at 0.1% level

adaptive. For this purpose the GCA's for all the characters (averaged over all generations) at Parkland were regressed for each of the parental lines upon those at Ellerslie. The regression coefficients and the sums of squares due to regression and error partitioned for each cultivar are given in Table 82. It may be pointed out that unweighted GCA's (original values) were used in regression analysis since the effect of change in the degree of expression of one character relative to the other can be studied regardless of the unit of scale used. Significance of mean squares due to regression (Table 82) indicates that for every unit of change in GCA's at Ellerslie there is a corresponding proportional change for the corresponding GCA's at Parkland.

The genetic components of variation (from unadjusted treatment means) D, F and H_1 were considered themselves as variables and factorially analysed over generations and locations in order to study their consistency over the two environments. Before performing the *factorial ANOVA*, the values of genetic components for each character were standardized at each location. Thus, each D value was divided by the V_{0L0} for the same character, generation and location. Similarly, F's were divided by their corresponding mean covariances (W_{0L01} in F_1 diallel, W_{0L02} in F_2 and backcross diallels and W_{0L03} in the selfed backcross diallel) and H_1's by their respective mean variances (V_{1L1} in F_1 diallel, V_{1L2} in F_2 and backcross diallels and V_{1L3} in the selfed backcross diallel). Thus, for example, the F for number of tillers per

TABLE 83

Factorial analysis of variance of genetic components of variation over generations and locations. The sum of squares are respectively partitioned for D, H_1 and F.

Component	Source of variation	D.F.	Sum of squares	Mean squares	F ratio
D	Locations	1	0.14331	0.14331	1.10820
	Generations	3	0.03167	0.01055	0.08164
	Location x Generation	3	0.07301	0.02433	0.18820
	Error	72	9.31106	0.12932	
H_1	Locations	1	10.38381	10.38381	7.77135***
	Generations	3	2.16681	0.72227	0.54056
	Location x Generation	3	1.10066	0.36688	0.27458
	Error	72	96.20391	1.33616	
F	Locations	1	15.78510	15.78150	7.34709***
	Generations	3	7.28304	2.42768	1.13021
	Location x Generation	3	0.43955	0.14651	0.06821
	Error	72	154.65565	2.14799	

***Significant at 0.1% level

plant at Ellerslie in the selfed backcross diallel set of Table 78 was divided by the corresponding V_{OL03} from Table 77 (at Ellerslie) as follows: -0.4873 ÷ 0.6890 = -0.7072.

The process of standardizing the scale is analogous to Allard's technique, where prior to *factorial ANOVA*, each variance and covariance was divided by V_{OLO} of the respective block for that character (Allard 1956; Crumpacker and Allard 1962). In the present study additive [D], dominance [H_1] and additive x dominance [F] components are subsequently considered separately and analysed independently for their stability over generations and locations. The reciprocals of the variances of the parents of the array mean variances and of the array mean covariances were used as weights in standardizing the values of D's, H_1's and F's respectively. The use of these different multipliers in normalizing the scale effects preserved the order of magnitude of respective parameters. The *factorial ANOVA* on the weighted values of D's, H's and F's is given in Table 83. The results show that additive effects of the genes (component D) are the same for two locations. Dominance gene effects (component H_1) and additive x dominance effects (component F) differ significantly at the two locations. On the whole, generations do not seem to affect the values of genetic components of variation. Significant mean squares for locations with respect to H_1 and F raises the question of the heterogeneity of location effects on the parameters in different generations. To answer this, the unweighted values of D's, H_1's and F's at Parkland were respectively regressed for each generation upon those of Ellerslie, and

TABLE 84

Analysis of variance of regression of genetic components of variation of Parkland upon those of Ellerslie for each generation.

Component	Generation	Source of variation	D.F.	Mean squares	F value	
Additive Component [D]	F_1 diallel	Due to regression	1	228657.5229	4578.6540***	r = 0.9990
		Due to error	8	49.9399		b = 1.0658
	F_2 diallel	Due to regression	1	227792.7663	3549.9323***	r = 0.9998
		Due to error	8	64.1682		b = 1.0603
	Backcross diallel	Due to regression	1	228207.7135	4597.8009***	r = 0.9990
		Due to error	8	49.6341		b = 1.0630
	Selfed backcross diallel	Due to regression	1	229349.4236	4251.7073***	r = 0.9990
		Due to error	8	53.9429		b = 1.0642
Dominance Component [H_1]	F_1 diallel	Due to regression	1	1532.9815	81.7304***	r = 0.9534
		Due to error	8	18.7562		b = 0.8233
	F_2 diallel	Due to regression	1	2001.8299	391.1351***	r = 0.9398
		Due to error	8	5.1180		b = 1.3637
	Backcross diallel	Due to regression	1	2619.8806	74.1992***	r = 0.9500
		Due to error	8	35.3087		b = 2.4385
	Selfed backcross diallel	Due to regression	1	412.1566	39.0566***	r = 0.9109
		Due to error	8	10.5528		b = 1.0823
Additive x dominance Component [F]	F_1 diallel	Due to regression	1	812.9743	80.8326***	r = 0.9538
		Due to error	8	10.0575		b = 0.4664
	F_2 diallel	Due to regression	1	1190.1414	31.2178***	r = -0.8921
		Due to error	8	38.1237		b = -1.4409
	Backcross diallel	Due to regression	1	40.3149	2.8143	r = 0.5100
		Due to error	8	14.3248		b = 0.3220
	Selfed backcross	Due to regression	1	8.6977	0.8605	r = 0.3098
		Due to error	8	10.1077		b = 0.3603

***Significant at 0.01% level

the sum of squares of deviations were partitioned into variation due to regression and remainder (error). Extremely high variance ratios (Table 84) for the parameters D and H_1, and close agreements between the coefficients of correlation and regression, both in sign and magnitude, indicate stability of these parameters over the two locations. The case of parameter F is rather confusing. The diallels based on backcross and selfed backcross generations show a lack of correspondence between F values at the two locations (variance ratio for regression non-significant). This may be ascribed to a change of relationship between additive and dominance gene effects ($F = \Sigma dh$) caused by altered environmental conditions. A more drastic relational change is that between the F_1 and F_2 generations of the diallel sets ($r = 0.95$, $b = 0.47$ and $r = -0.89$, $b = -1.44$, respectively). It is rather difficult to think of a logical explanation for this reversed relationship.

Since, on the whole, generation did not significantly affect the genetic components of variation, their estimates were obtained by solving, least-square-wise, the following system of linear equations, where the known terms, i.e., the array variances and covariances for a given generation were obtained by using adjusted treatment means from analysis of variance as a partially balanced lattice design:

(Parents): $D + E - V_{0L0} = d_1$

F_1 diallel: $(1/2)D - (1/4)F + (1/5)E - W_{0L01} = d_2$

TABLE 02

Components of genetic variation obtained from statistics based on adjusted treatment means for ten characters over four generations at two locations.

Character	D	F	H_1	H_2	E
Onset-of-heading	6.3274 ± 0.7633**	9.2901 ± 1.7240**	13.8477 ± 3.1078**	10.6407 ± 2.7703**	1.2748 ± 0.7546
	8.8228 ± 2.7613**	11.7407 ± 6.2367	24.7571 ± 11.2393	21.4808 ± 10.0215	3.7428 ± 2.7299
Final heading	9.0906 ± 1.4171**	15.6860 ± 3.2459**	18.0874 ± 5.8495**	12.6612 ± 5.2157*	1.6999 ± 1.4207
	7.8481 ± 3.7575	10.9021 ± 8.4867	20.9983 ± 15.2940	18.3467 ± 13.6368	3.6404 ± 3.7147
Heading-span	0.1776 ± 0.1378*	0.6367 ± 0.3118*	1.2987 ± 0.5612	0.9496 ± 0.5004	0.6144 ± 0.1361**
	0.5556 ± 0.0782**	1.7013 ± 0.1767**	4.6086 ± 0.3185**	3.4230 ± 0.2840**	0.4756 ± 0.0773**
Plant height	40.1849 ± 194.6123	-139.3000 ± 439.5492	-194.3500 ± 792.1188	-26.7551 ± 706.2076	329.6460 ± 192.3959
	15.6247 ± 324.5877	-384.9300 ± 733.1102	-274.4790 ± 321.1500	88.9778 ± 177.9948	324.0350 ± 320.8911
Number of tillers per plant	0.4516 ± 0.5333	1.3445 ± 1.2047	-1.0911 ± 2.1710	-1.5535 ± 1.9158	1.9733 ± 0.5273**
	1.4083 ± 0.1271**	1.9680 ± 0.2871**	6.3148 ± 0.5175**	5.3106 ± 0.4614**	0.2227 ± 0.1257
Number of spikelets per spike	0.7624 ± 0.1544**	1.1451 ± 0.3489*	0.8665 ± 0.6287	0.5013 ± 0.5606	0.5284 ± 0.1527**
	0.1911 ± 0.0819	0.2367 ± 0.1887	1.3766 ± 0.3402**	1.3117 ± 0.3033**	0.1653 ± 0.0826**
Number of seeds per spike	10.0189 ± 3.2757*	15.8223 ± 7.3986	26.7016 ± 13.3331	17.6712 ± 11.6084	13.0569 ± 3.2304**
	9.0831 ± 1.0313	19.5596 ± 2.3239**	45.8433 ± 4.1977	30.0795 ± 3.7429**	0.2803 ± 1.0495
Weight of seeds per spike	0.0139 ± 0.0025**	0.0146 ± 0.0056**	-0.0113 ± 0.0105	-0.0191 ± 0.0094**	0.0209 ± 0.0025**
	0.0194 ± 0.0071**	0.0369 ± 0.0161**	0.0239 ± 0.0291	0.0064 ± 0.0259	0.0170 ± 0.0070**
1000-kernel weight	5.0333 ± 1.2956**	7.6451 ± 2.9262**	11.5453 ± 5.2724	7.9758 ± 4.7020	3.9945 ± 1.2808*
	9.2436 ± 3.0167*	16.2749 ± 6.8136*	19.2289 ± 12.2769	11.4570 ± 10.9484	2.6962 ± 2.9024
Yield per plant	1.8082 ± 0.7141*	3.4832 ± 1.6130	4.9964 ± 2.9068	3.3320 ± 2.5918	2.5752 ± 0.7060**
	-1.1075 ± 0.1048**	-1.9481 ± 0.4400**	-4.3292 ± 0.7930**	-3.4484 ± 0.7071**	2.3649 ± 0.1926**

The first reading under each column refers to Ellerslie and the second to Parkland.
* Significant at 5% level
**Significant at 1% level

$$(1/4)D - (1/4)F + (1/4)H_1 + (3/5)E - V_{1L1} = d_3$$

$$(1/4)D - (1/4)F + (1/4)H_1 - (1/4)H_2 + (1/10)E - V_{0L1} = d_4$$

F_2 diallel:

$$(1/2)D - (1/8)F + (1/5)E - W_{0L02} = d_5$$

$$(1/4)D - (1/8)F + (1/16)H_1 + (3/5)E - V_{1L2} = d_6$$

$$(1/4)D - (1/8)F + (1/16)H_1 - (1/16)H_2 + (1/10)E - V_{0L2} = d_7$$

Backcross diallel:

$$(1/2)D - (1/8)F + (1/5)E - W_{0L02} = d_8$$

$$(1/4)D - (1/8)F + (1/16)H_1 + (2/5)E - V_{1I2} = d_9$$

$$(1/4)D - (1/8)F + (1/16)H_1 - (1/16)H_2 + (7/100)E - V_{0L2} = d_{10}$$

Selfed backcross diallel:

$$(1/2)D - (1/16)F + (1/5)E - W_{0L03} = d_{11}$$

$$(1/4)D - (1/16)F + (1/32)H_1 + (2/5)E - V_{1L3} = d_{12}$$

$$(1/4)D - (1/16)F + (1/32)H_1 - (1/32)H_2 + (7/100)E - V_{0L3} = d_{13}$$

In this system of equations $d_{K=1,2,\ldots,13}$ denotes the difference between the expected and observed values of the kth statistic. The environmental component of variation (E) was accounted for by using the multiplier ($1/2$) when F_1 and F_2 generations, and ($1/4$) when backcross and selfed backcross generation diallel sets were considered (Hayman 1958). The solutions of this system of equations for the various components of variation are shown in Table 85. Error terms were calculated in a manner usual to the **unweighted** least square solution, i.e. as $\pm (\sum_k d_k c_{ii} \div DF)^{1/2}$, where c_{ii} is the appropriate term on the main diagonal of the variance-covariance matrix of the coefficients,

TABLE 86

Estimates of genetic parameters from diallel analysis of adjusted treatment means for ten characters over four generation at two locations.

Character	$[H_1 \div D^{1/2}]$	$[H_2 \div 4H_1]$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}\right]$	Heritability
Onset-of-heading	1.4763*	0.1921*	2.9621*	0.3968
	1.6751	0.2169	2.3169	0.2689
Final heading	1.3455*	0.1750*	3.8012*	0.3674
	1.6356	0.2184	2.4948	0.2420
Heading-span	1.8545	0.1827	3.9680	0.1145
	2.8931*	0.1856*	3.2920*	0.1027
Plant height	2.1990	0.0344	0.1188	0.0308
	4.1886	-0.0810	-0.4922	0.0109
Number of tillers per plant	1.9543	0.3559	46.3456	0.0764
	2.1175*	0.2102*	1.9999*	0.2125
Number of spikelets per spike	1.0660	0.1446	5.7672	0.2935
	2.6839	0.2382*	1.6100	0.0960
Number of seeds per spike	1.7276	0.1642	2.8599	0.1386
	2.3135	0.1545	2.7392	0.2312
Weight of seeds per spike	0.9016	0.4225	3.7901	0.1941
	1.1099	0.0669	23.2285	0.2679
1000-kernel weight	1.5144	0.1727	3.0116	0.2020
	1.4422	0.1489	4.1330	0.4026
Yield per plant	1.6622	0.1667	3.7498	0.1327
	1.9770*	0.1991	0.3842	-0.1855

First reading under each column refers to Ellerslie and the second to Parkland
*The parameters involved are significantly different from zero (Table 85)

and D.F. = 13 - 5 = 8 (thirteen equations, five fitted parameters). For one set of paradoxical results (significant negative values of D, H_1 and H_2 for yield per plant at Parkland), the source of error could not be determined.

The proportional estimates of genetic parameters obtained from Table 85 are given in Table 86. The data indicate that all characters are inherited as over-dominant traits at both locations, except for weight of seeds per spike at Ellerslie which showed nearly complete dominance, i.e. $(H_1 \div D)^{1/2} = 1$. Moreover $[(1/4DH_1)^{1/2} + F] \div [(1/4DH_1)^{1/2} - F] > 1$ in all cases, except for plant height at both locations and yield per plant at Parkland, suggests strongly a preponderance of dominant genes in the parents. When valid, $(H_2 \div 4H_1)$ was found to be less than 0.25, indicating thus a certain degree of numerical asymmetry of alleles with positive and with negative effects at loci showing dominance. Heritability values in all cases were low, the maximum being 40.26% (1000-kernel weight at Parkland).

The results of Table 86 when compared with those of Tables 20, 39, 60 and 79 show the effect of the adjustment factor characteristic of incomplete block designs. In the latter Tables, where genetic parameters have been estimated from analyses of F_1, F_2, backcross and selfed backcross diallel sets of unadjusted treament means (treated as randomized block design), the values of $(H_1 \div D)^{1/2}$, $(H_2 \div 4H_1)$ and $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ show a wide range of variation from partial dominance to overdominance, from a fully symmetrical distribution of alleles with positive and negative effects to strong

TABLE 87

Analysis of variance of regression of genetic components of variation at Parkland upon those at Ellerslie averaged over generations for all characters.

Component of variation	Source of variation	D.F.	Sum of squares	Mean squares	Coefficients of correlation & regression
Additive component [D]	Due to regression	1	228499.9514	228499.9514**	b = 1.0633
	Due to error	8	432.9894	54.1236	r = 0.9990
Dominance component [H_1]	Due to regression	1	1561.3878	1561.3878**	b = 1.3188
	Due to error	8	65.5032	8.1879	r = 0.9796
Additive x Dominance Component [F]	Due to regression	1	306.8222	306.8222**	b = 1.0430
	Due to error	8	100.9412	12.6176	r = 0.8674
Additive component [D]	Due to regression	1	197.6459	197.6459**	b = 0.3825
	Due to error	8	90.3328	11.2916	r = 0.7579
Dominance component [H_1]	Due to regression	1	76528.1655	75528.1655**	b = 1.4230
	Due to error	8	345.5664	43.1958	r = 0.9997
Additive x Dominance Component [F]	Due to regression	1	137604.3889	137604.3889**	b = 2.6663
	Due to error	8	963.3961	120.4245	r = 0.9964

The first part of the table refers to unadjusted treatment means (treated in randomized block design) and the second part refers to adjusted treatment means from partially balanced lattice design.

**Significant at 1% level

asymmetry, and from equal to unequal proportions of dominant to recessive alleles in the parents. Table 86 on the other hand shows that these ratios, especially those for valid parameters (* in Table 85), are more stable over characters since over-dominance in inheritance, asymmetry of alleles at loci exhibiting dominance, and inequality in the proportions of dominant and recessive alleles are constant features of the concerned characters.

The regression analysis of genetic components of variation D, H_1 and F for Ellerslie and Parkland, obtained first from unadjusted treatment means (randomized block design) averaged over generations, and then from adjusted treatment means of Table 85, is given in Table 87. The purpose of this analysis was to see whether there is concordance between the values of parameters evaluated from the data at the two locations separately. The results given in Table 87 show a good agreement in this respect between locations. Parameters D and F evaluated from array variances and covariances from unadjusted treatment means show the same rates of change from character to character at the two locations ($b \approx 1$). For H_1 this change is $b = 1.32$ at Parkland for unit change at Ellerslie. With adjustment of treatment means the situation is changed, so that for unit change at Ellerslie there is a change of $b = 0.38$ for D and $b = 2.67$ for F at Parkland. The corresponding change for H_1 is less pronounced ($b = 1.32$) without adjustment as compared to $b = 1.42$ with adjustment.

The relationships between the two locations in regard to changes in D, H_1 and F for the various characters are shown graphically

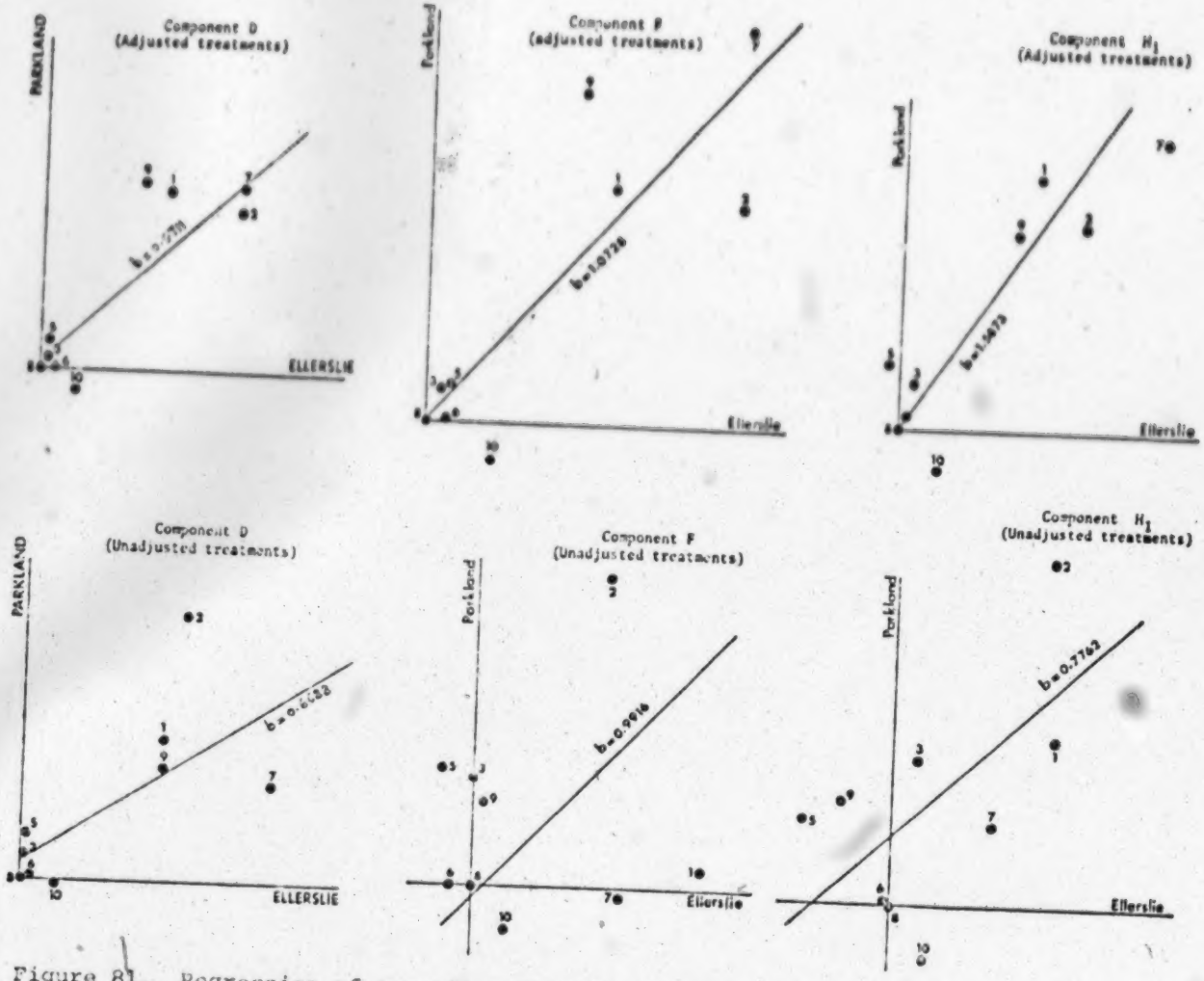

Figure 81. Regression of genetic components of variation at Parkland upon those at Ellerslie for all the characters except plant height. Solid circles refer to regression intercepts for different characters.

in Figure 81. The scatter of the intercept points around the regression lines shows that there are considerable discrepancies between the two locations. The points of intercepts for plant height are not shown in the graphs because of very high values of the components which far exceeded the boundaries of the graphs. Therefore the coefficients of regression were recalculated excluding plant height. It is rather difficult to determine either from the regression analysis of Table 87 or from the graphs whether and by how much the use of adjusted treatment means has improved the estimates of the parameters. Hence it is not possible to assess the parametric relationships within and between the characters and within and between the locations or environments. Nevertheless, looking at the graphs of the parameters derived begining with the adjusted traetment means, one would be rather strongly inclined to conclude that the adjustment of means has considerably improved the degree of concordance between the two locations with respect to parameters.

DISCUSSION

The F_1, F_2, backcross and selfed backcross generations of five parent diallel cross of common wheat (*Triticum aestivum* L.) were grown in 1972 at two locations and the data obtained was analysed with respect to correlation between the characters, principal factors, general and specific combining abilities, genetic components of variation and environmental effects. The experimental design used was a partially balanced triple lattice. However, most of the analyses were carried out both as a complete randomized block design and as a lattice design. The results obtained are discussed in sequel.

Correlation and factor analyses. Among the characters considered in this study, yield of grain per plant is agronomically the most important. Therefore the knowledge of its correlation with other characters is of importance from a theoretical and a practical point of view. The results of the correlation analyses of F_1, F_2, backcross and selfed backcross diallel sets are given in Tables 2, 21, 42, and 61. These results show that early maturing entries have produced high yields and the late maturing ones low yields of grain per plant. As expected, there was a positive correlation between yield per plant and most of its subcharacters or components. A strong positive association was found to exist between the subcharacters, number of tillers per plant, weight of seeds per spike and 1000-kernel weight with yield per plant. The components, number of spikelets per spike and number of seeds per spike were not correlated with yield at either location in F_1 (Table 2) but were

positively correlated in the other generations of diallel cross either at both locations (Table 21) or at one of them (Tables 42 and 61). There was no correlation between yield and plant height.

The degree of expression of metrical characters (phenotypes) depends both on the genotypic constitution of the parents and the environmental conditions under which the experimental materials are grown. Therefore the comparison of results obtained by various researchers using different sets of parents and carried out under different environmental conditions lead only to non-related or loosely-related general information. For example, Lee and Kaltsikes (1973) working with durum wheat in Winnipeg have found that the characters days-to-maturity and yield per plant were positively correlated in both the F_1 and the F_2 generations of a 10 x 10 diallel cross, whereas in the present study of all the generations of diallel cross the correlation was negative. On the other hand, Hsu (1970) has found that in the F_1 generation of a five-parent diallel cross of common wheat there was no correlation between anthesis date (final heading) and yield per plant, a result similar to that found in the present case at Parkland. Although Hsu has conducted his study in Edmonton, the two experiments were spaced in time, and except for Inia, the parental lines used were different. The significant positive association of yield per plant with its components found in this study was also observed in the works of Johnson and Schmidt (1968), Smocek (1969), Lebsock and Amaya (1969), Hsu and Walton (1970), Kaltsikes and Lee (1971), Lee and Kaltsikes (1973) and Chebib *et al* (1973). The absence of correlation between plant height

and yield per plant in the present study was also observed by Kaltsikes and Lee (1971) and Chebib *et al* (1973). These results are in disagreement with those of some other experiments [Lebsock and Amaya (1969), Kaltsikes and Larter (1970) and Lee and Kaltsikes (1973)].

The relationship between individual character is rather complicated. Therefore the data were subjected to factor analysis. This analysis provides information on contributions of independent variables relative to those of dependent ones. The results of the factor analysis of F_1, F_2, backcross and selfed backcross data obtained for two locations are shown in Tables 3, 22, 43 and 62, and the principal factors have been interpreted earlier. The first principal factor, *lateness*, has negative loading for yield per plant and the highest positive loading for onset-of-heading and final heading. This confirms the conclusion arrived at earlier, that the majority of late-heading entries have produced low grain yields per plant. The degree of expression of heading-span was found to be correlated with final heading but not with onset-of-heading. It was not correlated with yield in F_1 and F_2 but was positively associated with it in backcross and selfed backcross data. This inconsistency suggests that heading-span is not one of the characters affecting yield per plant. In fact the factor analyses based on the F_1, F_2 backcross and selfed backcross diallel sets have revealed positive factor loadings for heading-span and negative ones for yield. It follows therefore that positive correlations of heading-span with yield per plant at Parkland in the backcross and selfed backcross diallel sets does not necessarily imply

a cause-and-effect relationship, and may in fact be attributed to strong environmental influence upon particular entries of the diallel table.

The second principal factor, termed differently in different generations, carried the highest loadings for number of spikelets per spike, number of seeds per spike and weight of seeds per spike except the backcross diallel at Parkland (Table 43), for which plant height had the highest loading. A similar situation was observed with respect to principal factors 3, 4 and 5 which had their highest loadings from different characters in different generations of the diallel cross. Thus it appears that different factors operate differently in different populations (generations) though they share the same gene pool.

Combining ability analyses. The results of the analyses of data for general and specific combining abilities with respect to the characters considered have shown that the parents with high GCA's do not necessarily produce hybrids with high SCA's. The comparisons of GCA's with SCA's for all the generations and characters are collected in Table 88. Of all the comparisons, eighty to be exact, 84% constitute cases in which high SCA's are associated with one or both parents having low GCA's, and *vice versa*. These observations are in agreement with those reported by Crumpacker and Urquhart (1962), Fonseca (1965), Brown *et al* (1966), Gyawalli *et al* (1968) and Singh *et al* (1969) in wheat. Analogous results have been observed by Larson (1941) in tomatoes, and

TABLE 58

Summary of the results of general and specific combining ability analyses showing that the hybrids with highest SCA's are associated with parents of low GCA's and *vice versa*.

		Onset-of-heading				Final heading				Heading-span				Plant height				Number of tillers per plant			
		F1	F2	BO	B1	F1	F2	BO	B1	F1	F2	BO	B1	F1	F2	BO	B1	F1	F2	BO	B1
	*Both parents with high GCA									+-				++	+-			+-			
Hybrid with highest SCA	One parent with low GCA				-+	++			+-	-+	++	++	++		-+	++	++		++		++
	Both parents with low GCA	++	++	++	-+		++	++	-+									-+		++	
	Both parents with high GCA				++									++	++			-+			
Hybrid with lowest SCA	One parent with high GCA	++	++	++		++	++	++	++	++	++	++	++			++	++	-+	++	++	++
	Both parents with low GCA																				

		Number of spikelets per spike				Number of seeds per spike				Weight of seeds per spike				1000-kernel weight				Yield per plant			
		F1	F2	BO	B1	F1	F2	BO	B1	F1	F2	BO	B1	F1	F2	BO	B1	F1	F2	BO	B1
	*Both parents with high GCA	-+	-+	+-	-+																
Hybrid with highest SCA	One parent with low GCA	+-	+-	-+	+-			+-		-+	++	++		++	++	++	++	++	++	-+	++
	Both parents with low GCA					++	++	-+	++	+-			++							+-	
	Both parents with high GCA					++								++	+-			+-	-+		
Hybrid with lowest SCA	One parent with high GCA	++	++	++	++	++		++	++	+-	-+	-+	-+	-+	-+	++	++	-+	+-	++	++
	*Both parents with low GCA									-+	+-	+-	+-								

(+) and (-) signs indicate, respectively, affirmation and contradiction of the statements.
The first position of (+) or (-) refers to Ellerslie and the second to Parkland.
*(+) sign characteristic of the location shows disagreement of the proposition made in the text.
F1, F2 BO and B1 refer to F_1, F_2, backcross and selfed backcross generations of diallel set.

by Walker (1963), Chang (1967), Soomro (1967), Baluch and Soomro (1969) and Soomro and Baluch (1969) in cotton. On the other hand Kime (1950) and Hawkins *et al* (1965) working with cotton have found that GCA and SCA were positively correlated so that the present results are in contradiction to their reports.

Significant variances of general and specific combining abilites for a particular character denote, respectively, the importance of additive and non-additive gene effects for that character. If the variance for specific combining ability for a particular character is significant and that for general combining ability is not, selection for the character will be on the basis of SCA. On the other hand, high SCA variances associated with a particular parent, even if it has high GCA, reflect an insonsistency in the performance of that parent with respect to the particular character (Griffing, 1956) and indicate that the hybrids involved with that parent would perform poorer than would be expected on the basis of their specific combining abilities. It follows therefore that in combining ability screening tests a pedigree selection procedure would be expected to screen out the strains with considerably larger SCA variances.

In the present studies variances of general combining ability were generally larger than those of specific combining ability for all characters, and diallel-set generations at both locations (Tables 5 to 14, 24 to 33, 45 to 54 and 64 to 73). There were a few cases where the estimates of SCA variances were higher than those for GCA's, but the magnitudes of their differences were negligible. This

would indicate a high consistency of performance of the parental lines an observation which may also be generally verified by their general combining ability values (Tables 4, 23, 44 and 63), and more specifically from the results of Table 82. The significance of variances for general and specific combining abilities were examined from Tables 15, 34, 55 and 74. In general, the mean squares for GCA were significant for all characters except heading-span and yield per plant at one or both the locations. Such significances of GCA mean squares are not uncommon in wheat (Brown *et al* 1966, Fonseca 1965, Paroda and Joshi 1970a, Parodi *et al* 1970 and Bitzer *et al* 1971). Mean squares for SCA were significant only for a few characters.

It may be pointed out that a high general combining ability for some characters as for example onset-of-heading and final heading may not be desirable under certain circumstances. High GCA for these characters implies lateness, so that when selecting for earliness, lines with the lowest GCA's must therefore be given priority. In the present study Ciano and Inia had the lowest GCA's for heading data, and consequently selection from their progenies is expected to result in early lines. Plant height is another character for which the selection of wheat cultivars with low GCA's may be desirable.

Diallel cross analysis. The analysis of variance of diallel tables according to Hayman (1954a) gave *a* component significances (for additive gene effects) in all generations of the diallel cross (Tables 16, 35, 56 and 75) for all the characters except heading-span and yield per plant

(Tables 16 and 35) and yield per plant (Tables 56 and 75). These results corresponded to those for general combining ability in *ANOVA*'s (Tables 15, 34, 55 and 74). Thus Hayman's a component and Griffing's GCA are analogous. Genetic components of variation for each generation of the diallel cross have shown values ranging from non-significance to high significance. The only paradoxical ones are the negative but significant D's and H_1's of Tables 19, 38, 59 and 78, which may be ascribed to high environmental variation. Such unexpected values are not uncommon (Mather 1949, Wright 1952, Newell 1970 and Holmes 1972) in biometrical genetics. The interpretation of genetic parameters in such cases becomes questionable.

Proportional values of the estimates of genetic parameters viz., $(H_1 \div D)^{1/2}$, $(H_2 \div 4H_1)$, $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ and $[h^2/H_2]$ for characters studied in different generations of the diallel cross ranged from partial dominance to over-dominance, from complete symmetry to strong asymmetry in distribution of genes with positive and negative effects in the parents, from equal proportions of dominant and recessive genes in the parents to a preponderance of dominants or recessives, and from high to low nurbers of gene groups controlling a particular character. Heritability estimates also showed a wide range of values, from -0.1129 (yield per plant, Table 39) to +1.085 (onset-of-heading, Table 79), indicating in this example, a complete lack of heritability for yield and an extremely high heritability for earliness. Quite low heritability estimates of yield in wheat have been reported by a number of researchers (Wiebel 1956, McNeal 1960,

Kronstad and Foot 1964, Johnson *et al* 1966, and Paroda and Joshi 1970, 1970a).

Genotype-environment interaction. The assessment of genetic and environmental components of variation with respect to a character depends upon the gene pool involved and the non-hereditary factors constituting the environment in which the experimental material is grown. The choice of statistical approach varies with the type of data available and the object of the study. In this study *factorial ANOVA* and regression analysis (Mather, 1951) were used to assess the degree of discordance between identical sets of materials grown at two locations with respect to factor loadings for the various characters, general combining abilities of the parents and the main genetic components of variation.

The factor loadings on various characters seemed to be different for the two locations (Table 80). The effect of generations on factor-loading scores for different characters was negligibly small. In fact none of the interactions involving generation were significant. This finding contradicts that of Lee and Kaltsikes (1973) who found discrepancies between their F_1 and F_2 diallel factor analyses with respect to the factor loading scores on various characters. They attributed these generation differences to a considerable difference in plot size for the two generations, and difference in planting techniques viz., space-planting for F_1 diallel and solid planting for F_2 diallel. In the present case, though plot size, planting techniques and experimental

set up was the same, nevertheless, the environmental conditions at the two locations were quite different. Inspite of significant inter-location effects, different generations proved to be fairly homogeneous with regard to factor loadings.

In the *factorial ANOVA* for general combining abilites of the four generations of the diallel cross and the two locations (Table 81) it was found that the GCA values were more or less the same. However, when characters were treated separately in the analysis (*ANOVA* assumed single observation per cell), GCA's differed between locations. These results indicate that parents did not differ in GCA's over the two locations when their GCA's were averaged over all characters, but they certainly did when considered individually for each character. The response of each variety with respect to additive gene effects was studied after averaging the GCA's of a cultivar over four generations of the diallel cross and regressing the estimates obtained at one location upon those of the other. In the analysis of variance for regression (Table 82) the inter-location effects were found to be homogeneous for each variety. In other words, the GCA's for the two locations were concordant. The variances for general and specific combining ability also did not differ significantly at the two locations. Moreover, the conspicuous feature of the combining ability analysis was the high consistency with which the GCA variances were higher than the corresponding SCA variances at both locations. This in fact shows the stability of cultivars over locations according to Griffing's (1956) enunciation.

The stability of genetic components of variation, viz., D, H_1 and F was assessed over the two locations through *factorial ANOVA*. The results indicated (Table 83) that there was no significant difference between locations for any component. Moreover, the generations, on the whole, did not affect these parameters at either location. But when the estimates of one component for Parkland were regressed upon those of Ellerslie it was found that the selfed backcross generation of the diallel cross was affecting the component F. This constituted a significant change in the relationship between additive and dominance gene effects in the progeny of the backcrosses. Moreover the estimates of the F component for the two locations were correlated differently in the F_1 and F_2 generations ($+r$ and $-r$ respectively). It is rather difficult to think of a logical explanation for this change of relationship between additive and dominance gene effects [$\Sigma(d) \times \Sigma(h)$] in two generations of the same diallel set.

The occurrence of significant negative values for genetic components of variation was an unexpected feature of diallel cross analysis for which a satisfactory interpretation is lacking. Such values have been reported in a number of instances (Mather 1949, Wright 1952, Newell 1970 and Holmes 1972) but a logical explanation for their occurrence has not been given. The frequency of their occurrence appear to be too high to be attributed to chance.

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APPENDIX I

Origin, parentage and varietal description
of five cultivars of wheat used in diallel study

Variety:	Marquis
Origin:	Central Experimental Farm, Ottawa, Canada
Parents:	Hard Red Calcutta x Red Fyfe
Growth habit:	Spring
Plant height:	110 - 120 cms.
Spike:	Mid-long, fusiform with apical awns; beaks short, acute
Kernel:	Dark red, hard, ovate-truncate

Variety:	Chinook
Origin:	Central Experimental Farm, Ottawa, Canada
Parents:	Thatcher x S-615-11
Growth habit:	Spring
Plant height:	110 - 125 cms.
Spike:	Fusiform, mid-long, short apical awns, white glumes with mid-wide beaks
Kernel:	Red, hard, short to mid-long, oval

Variety:	Khush-hal
Origin:	Agricultural Research Institute, Peshawar, Pakistan
Parents:	Local white x Standard Desi
Growth habit:	Spring
Plant height:	80 - 90 cms.
Spike:	White, flufy, awned, white pubiscent glumes with mid-wide beaks
Kernel:	Amber colored, soft, mid-long, oval

Variety:	Ciano-67
Origin:	National Institute of Agricultural Research, Mexico
Parents:	Pitic 62-Chris 'Sib' x Sonora 64
Growth habit:	Spring
Plant height:	85 - 95 cms.
Spike:	White, bearded, fusiform
Kernel:	Hard red, medium size

Variety:	Inia-66
Origin:	National Institute of Agricultural Research, Mexico
Parents:	Lerma Rojo 64 x Sonora 64
Growth habit:	Spring
Plant height:	100 - 110 cms.
Spike:	White, bearded, fusiform
Kernel:	Hard, red, medium-long

APPENDIX-II

NUMERICAL DESIGNATIONS OF THE PARENTS AND THEIR CROSSES USED IN THE DIALLEL ANALYSES

1. (KxCH)F22	46. (CHxI)I1	91. I-PARENT	136. K1(CxK)	181. (CxK)F2
2. (IxK)I1	47. C-PARENT	92. (CxK)C1	137. (MxCH)M1	182. (IxC)F22
3. I1(IxC)	48. (CxK)F22	93. CH0(MxCH)	138. (CxI)F2	183. CH0(CHxC)
4. (KxM)F22	49. (CHxI)CH0	94. CH1(CxCH)	139. I0(KxI)	184. (IxCH)I1
5. (IxC)I1	50. (KxI)I1	95. C1(CxM)	140. C0(MxC)	185. (CHxC)C1
6. (CxI)F22	51. (CHxI)F2	96. (IxM)I1	141. (CHxK)F1	186. I0(IxM)
7. CH1(MxCH)	52. C1(IxC)	97. (MxCH)CH1	142. (IxC)C1	187. I0(CHxI)
8. (IxK)F2	53. (KxM)K0	98. M1(CxM)	143. M1(IxM)	188. (KxC)C0
9. M-PARENT	54. (KxM)M0	99. (CxCH)CH1	144. C0(KxC)	189. (IxCH)F1
10. K1(FxCH)	55. M0(MxC)	100. (CxCH)F2	145. (CHxC)F2	190. (KxI)I0
11. (CxI)C1	56. (MxI)F22	101. C0(IxC)	146. K0(IxK)	191. C0(CHxC)
12. (MxK)M0	57. I0(IxC)	102. K1(KxI)	147. (CxM)C1	192. (CxM)C0
13. K1(CHxK)	58. (MxC)C0	103. (KxC)K0	148. (MxCH)F22	193. (KxM)F1
14. (CHxM)CH1	59. (CHxM)F2	104. (MxC)F22	149. K0(CxK)	194. (CHxC)CH0
15. C1(CHxC)	60. CH1(CHxM)	105. (KxCH)CH0	150. (MxI)F1	195. (IxM)I0
16. K-PARENT	61. (CHxC)F22	106. C1(MxC)	151. (KxI)F2	196. (IxCH)I0
17. (IxK)K1	62. M0(CHxM)	107. CH-PARENT	152. CH1(KxCH)	197. CH0(MxCH)
18. CH1(CHxK)	63. (MxC)F2	108. C1(CxK)	153. C0(CxCH)	198. M1(MxK)
19. (KxCH)F2	64. M0(IxM)	109. (CHxK)CH1	154 (M..)K0	199. I0(IxK)
20. CH1(CHxC)	65. (IxCH)CH0	110. (MxCH)M0	155. M1(CHxM)	200. (MxC)M0
21. (MxK)M1	66. (KxI)F22	111. M1(MxCH)	156. K0(MxK)	201. I1(CHxI)
22. I1(IxK)	67. (CxM)M0	112. (MxI)M1	157. (MxCH)CH0	202. (KxI)I0
23. C1(CxCH)	68. (CxI)C0	113. (CxM)F2	158. (MxCH)F1	203. (CxK)C0
24. (KxC)F2	69. (KxC)C1	114. (CHxM)CH0	159. K1(IxK)	204. (IxC)F1
25. (MxK)F22	70. (CxCH)CH0	115. (IxK)F1	160. (IxC)C0	205. (CHxC)F1
26. (IxK)F22	71. M1(MxC)	116. (CHxK)K0	161. (CxM)M1	206. I1(IxCH)
27. (CHxC)CH1	72. K0(KxI)	117. (CHxI)F22	162. C0(CxM)	207. K0(KxCH)
28. CH1(CHxI)	73. (CHxI)CH1	118. (IxK)I0	163. CH0(CHxK)	208. M0(CxM)
29. I1(KxI)	74. (CxK)K1	119. I1(MxI)	164. (FxI)K1	209. (IxC)I0
30. (IxCH)CH1	75. (MxI)I0	120. M1(KxM)	165. CH0(CHxI)	210. (CHxK)F22
31. K1(KxC)	76. (CHxM)M1	121. (MxC)C1	166. M1(MxI)	211. (CHxI)I0
32. (CxI)I1	77. (CxCH)C1	122. (IxM)M1	167. C0(CxK)	212. CH0(CxCH)
33. (CxK)F1	78. (CHxM)F22	123. CH0(CHxM)	168. (CxM)F1	213. K1(KxM)
34. CH1(IxCH)	79. I0(MxI)	124. (KxM)K1	169. (KxM)F2	214. (CxI)I0
35. (CHxC)C0	80. (MxCH)F2	125. (IxM)F1	170. I0(IxCH)	215. (KxI)F1
36. K0(KxM)	81. M0(MxM)	126. M0(MxK)	171. K1(MxK)	216. (MxC)F1
37. (IxM)F2	82. (KxCH)K1	127. (MxC)M1	172. (IxC)F2	217. M0(MxI)
38. (CHxK)K1	83. I0(CxI)	128. I1(IxM)	173. (CxI)F1	218. K0(KxC)
39. (IxK)K0	84. (MxK)F2	129. (MxI)F2	174. M0(MxCH)	219. C0(CxI)
40. (KxM)M1	85. (CxCH)F1	130. K0(CHxK)	175. (CxCH)F22	220. (MxK)F1
41. (KxC)F1	86. (CHxM)M0	131. (IxCH)F2	176. (CHxM)F1	221. (CxCH)C0
42. (KxC)F22	87. (IxCH)F22	132. (MxC)K1	177. (MxI)I1	222. (CxI)I0
43. (CHxK)F2	88. CH0(IxCH)	133. C1(CxI)	178. (KxCH)CH1	223. (KxCH)F1
44. (CHxC)CH0	89. (MxK)K1	134. (CxM)F22	179. I1(CxI)	224. (KxCH)K0
45. (IxM)M0	90. (IxM)F22	135. C1(KxC)	180. (MxK)K0	225. (CHxI)F1

NOTE: M=Marquis, CH=Chinook, K=Khush-hal, C=Ciano-67 and I=Inia-66.
Taking any two varieties, for example 'C' and 'K', above mentioned combinations could be explained as follows:

(CxK)F1 = F_1 hybrid.
(KxC)F1 = Reciprocal F_1 hybrid.
(CxK)F2 = F_2-generation hybrid.
(KxC)F2 = Reciprocal F_2 hybrid.
(CxK)F22 and its reciprocal are the F_2's repeated second time in each replication to complete the requirements of the 15x15 partially balanced lattice design.

(CxK)C0 = Back cross-1.
C0(CxK) = Reciprocal back cross.
(CxK)K0 = Back cross-2.
K0(CxK) = Reciprocal back cross-2.
(CxK)C1 = Selfed generation of (CxK)C0.
C1(CxK) = Reciprocal of (CxK)C1.
(CxK)K1 = Selfed generation of (CxK)K0.
K1(CxK) = Reciprocal of (CxK)K1.

APPENDICES III TO XXII

Unadjusted treatment means (original data) of all the entries with respect to ten quantitative characters at two locations.

The numbers in the first row of each block are the code numbers of entries and those in the second row are the mean values of the corresponding entries listed in Appendix II .

APPENDIX III Onset-of-heading at Ellerslie

ELLERSLIE REPLICATION-1.

(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	50.000	51.000	54.000	54.000	51.000	53.000	52.000	53.000	53.000	53.000	52.000	52.000	54.000	54.000	52.000
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2.	52.000	52.000	57.000	52.000	53.000	54.000	53.000	53.000	52.000	52.000	54.000	55.000	54.000	53.000	55.000
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	51.000	51.000	53.000	53.000	53.000	52.000	53.000	53.000	52.000	55.000	52.000	52.000	54.000	55.000	54.000
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	53.000	49.000	51.000	53.000	52.000	53.000	49.000	53.000	54.000	52.000	52.000	51.000	52.000	57.000	57.000
	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140
5.	51.000	57.000	52.000	52.000	57.000	56.000	55.000	53.000	57.000	52.000	53.000	52.000	52.000	53.000	53.000
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	54.000	54.000	54.000	52.000	54.000	55.000	57.000	51.000	54.000	53.000	53.000	51.000	52.000	53.000	52.000
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	51.000	51.000	54.000	53.000	52.000	53.000	57.000	53.000	51.000	51.000	53.000	53.000	51.000	52.000	54.000
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	53.000	54.000	51.000	53.000	52.000	52.000	52.000	53.000	51.000	53.000	54.000	52.000	54.000	54.000	52.000
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	53.000	55.000	52.000	52.000	57.000	54.000	54.000	54.000	52.000	52.000	57.000	53.000	53.000	51.000	53.000
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	54.000	52.000	52.000	51.000	51.000	51.000	55.000	51.000	49.000	52.000	53.000	54.000	52.000	53.000	52.000
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	52.000	54.000	54.000	53.000	52.000	52.000	53.000	52.000	52.000	53.000	55.000	53.000	52.000	52.000	54.000
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	53.000	54.000	51.000	54.000	52.000	54.000	53.000	53.000	54.000	57.000	53.000	54.000	51.000	52.000	55.000
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	52.000	57.000	54.000	53.000	55.000	54.000	52.000	53.000	51.000	52.000	52.000	51.000	52.000	52.000	54.000
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	54.000	51.000	57.000	51.000	57.000	55.000	55.000	51.000	52.000	54.000	54.000	52.000	53.000	57.000	54.000
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	54.000	52.000	54.000	54.000	53.000	52.000	52.000	51.000	48.000	52.000	46.000	53.000	54.000	51.000	53.000

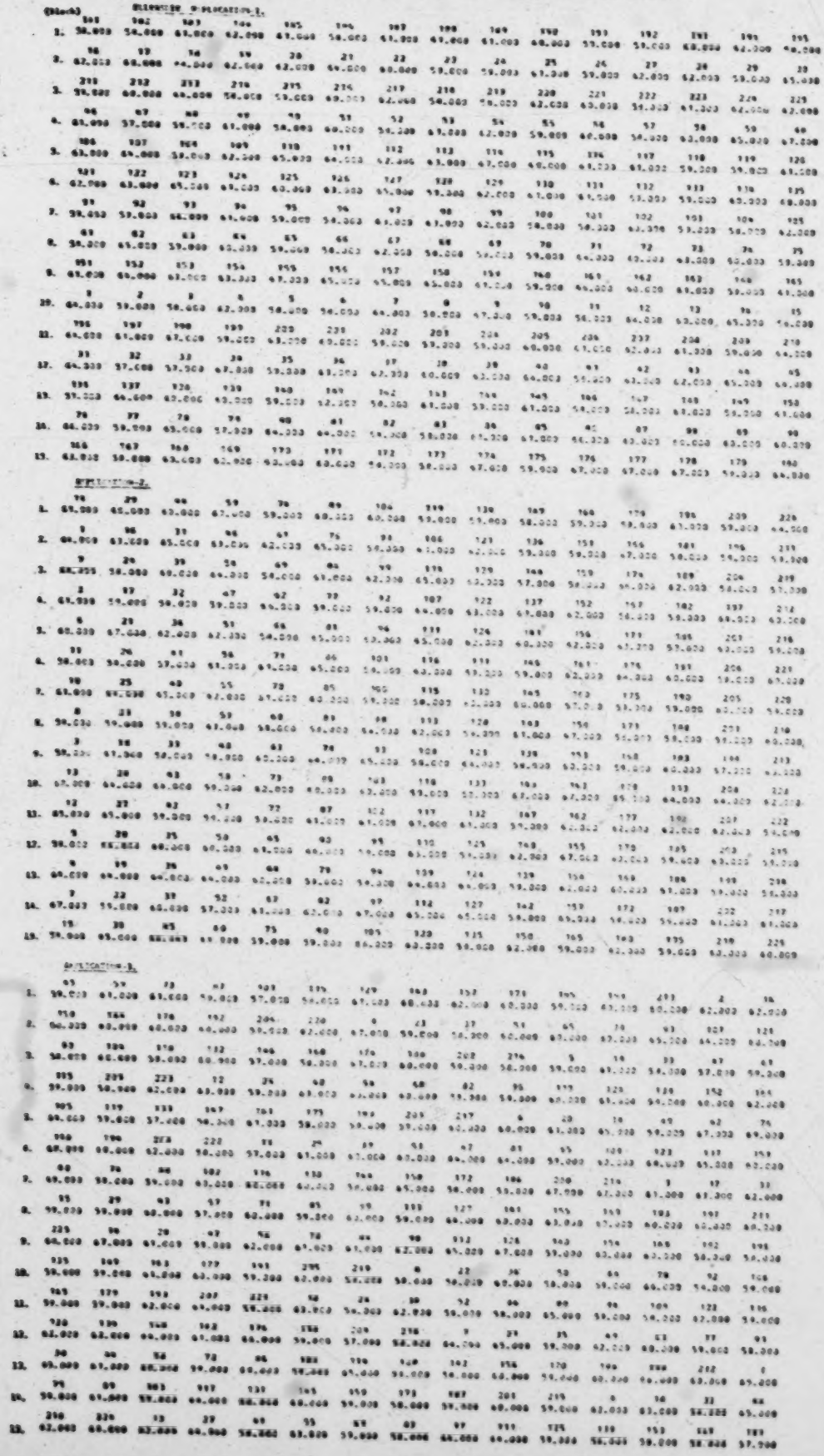
REPLICATION-2.

	16	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	59.000	54.000	51.000	57.000	52.000	53.000	54.000	52.000	53.000	52.000	52.000	52.000	56.000	52.000	54.000
	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
2.	55.000	57.000	53.000	53.000	52.000	54.000	52.000	52.000	56.000	51.000	52.000	55.000	51.000	52.000	51.000
	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
3.	60.000	52.000	53.000	56.000	50.000	54.000	54.000	57.000	53.000	52.000	52.000	57.000	54.000	54.000	51.000
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	51.000	50.000	52.000	52.000	54.000	52.000	52.000	54.000	56.000	54.000	54.000	52.000	49.000	57.000	54.000
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	53.000	57.000	55.000	55.000	53.000	54.000	53.000	54.000	54.000	54.000	54.000	54.000	53.000	53.000	53.000
	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
6.	51.000	52.000	52.000	53.000	53.000	57.000	52.000	53.000	52.000	53.000	54.000	57.000	52.000	52.000	54.000
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	58.000	53.000	54.000	53.000	57.000	53.000	52.000	51.000	53.000	53.000	57.000	52.000	52.000	54.000	55.000
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	52.000	53.000	53.000	54.000	52.000	52.000	57.000	54.000	53.000	53.000	56.000	52.000	52.000	52.000	53.000
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	51.000	54.000	52.000	52.000	53.000	57.000	57.000	52.000	54.000	54.000	52.000	52.000	52.000	53.000	54.000
	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
10.	51.000	54.000	53.000	53.000	54.000	52.000	52.000	53.000	53.000	58.000	54.000	55.000	55.000	53.000	54.000
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	56.000	53.000	52.000	52.000	52.000	53.000	53.000	53.000	52.000	52.000	54.000	53.000	53.000	53.000	52.000
	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
12.	52.000	53.000	53.000	52.000	53.000	57.000	52.000	57.000	52.000	52.000	57.000	53.000	52.000	52.000	53.000
	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214
13.	55.000	55.000	53.000	53.000	54.000	52.000	53.000	54.000	52.000	52.000	52.000	53.000	53.000	52.000	53.000
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	60.000	52.000	53.000	52.000	52.000	55.000	54.000	55.000	57.000	52.000	55.000	54.000	52.000	53.000	54.000
	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225
15.	53.000	55.000	53.000	59.000	53.000	53.000	58.000	53.000	52.000	54.000	54.000	53.000	53.000	53.000	54.000

REPLICATION-3.

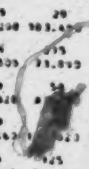
	45	59	73	87	101	115	129	143	157	171	185	199	213	2	16
4.	52.000	54.000	54.000	52.000	52.000	52.000	53.000	52.000	54.000	53.000	52.000	52.000	52.000	52.000	52.000
	150	164	178	192	206	220	8	23	37	51	65	79	93	107	121
2.	51.000	54.000	51.000	53.000	52.000	54.000	54.000	52.000	53.000	53.000	52.000	52.000	57.000	54.000	54.000
	90	104	118	132	146	160	174	188	202	216	5	19	33	47	61
3.	52.000	52.000	52.000	53.000	52.000	52.000	55.000	53.000	53.000	52.000	55.000	54.000	51.000	53.000	53.000
	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
4.	53.000	57.000	55.000	54.000	52.000	57.000	55.000	53.000	52.000	53.000	57.000	53.000	52.000	55.000	54.000
	135	119	133	147	161	175	189	203	217	6	29	34	48	62	76
5.	53.000	52.000	55.000	54.000	57.000	49.000	52.000	54.000	51.000	52.000	52.000	54.000	51.000	57.000	61.000
	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
6.	54.000	54.000	54.000	52.000	50.000	54.000	52.000	53.000	57.000	57.000	52.000	52.000	54.000	57.000	53.000
	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31
7.	58.000	58.000	53.000	54.000	53.000	53.000	52.000	57.000	49.000	52.000	57.000	57.000	57.000	57.000	57.000
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	50.000	52.000	53.000	53.000	53.000	52.000	53.000	52.000	57.000	52.000	54.000	53.000	52.000	54.000	52.000
	225	15	29	43	56	70	84	98	112	126	140	154	168	182	196
9.	54.000	54.000	54.000	52.000	54.000	57.000	54.000	54.000	57.000	58.000	52.000	54.000	54.000	51.000	52.000
	185	149	163	177	191	205	219	4	23	35	50	64	78	92	106
10.	52.000	51.000	53.000	53.000	52.000	52.000	52.000	52.000	51.000	51.000	54.000	52.000	54.000	52.000	54.000
	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
11.	52.000	52.000	55.000	53.000	52.000	53.000	52.000	53.000	51.000	52.000	57.000	53.000	52.000	53.000	52.000
	120	135	148	163	176	190	204	218	7	21	35	49	63	77	91
12.	54.000	52.000	55.000	52.000	58.000	52.000	52.000	52.000	57.000	57.000	52.000	54.000	54.000	52.000	52.000
	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
13.	55.000	51.000	52.000	57.000	58.000	52.000	57.000	54.000	52.000	53.000	53.000	54.000	57.000	52.000	54.000
	75	89	103	117	131	145	159	173	187	201	215	6	18	32	46
14.	52.000	53.000	53.000	55.000	52.000	51.000	54.000	53.000	53.000	52.000	54.000	54.000	54.000	53.000	55.000
	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	54.000	51.000	53.000	57.000	52.000	53.000	51.000	52.000	57.000	55.000	52.000	52.000	52.000	53.000	54.000

APPENDIX IV Final heading at Ellerslie



APPENDIX V Heading-span at Ellerslie

APPENDIX VI Plant height at Ellerslie



BALANCED REPLICATION-1 PLANT HEIGHT

(Block)	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155
1.	72.500	67.900	105.330	85.650	85.450	71.310	95.690	85.260	98.980	88.350	111.000	110.240	103.290	95.330	78.230
	96	97	98	99	20	21	22	23	24	25	26	27	28	29	30
2.	76.950	90.270	108.730	93.200	103.600	111.300	69.920	83.000	76.830	101.360	94.650	112.960	109.000	75.710	106.920
	217	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	83.500	89.250	89.570	72.500	93.850	84.340	103.140	71.600	75.240	96.540	95.140	76.750	93.590	97.440	92.160
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	94.030	81.980	99.170	114.520	[illegible]	104.770	86.260	114.950	122.640	93.230	101.330	76.220	104.620	125.310	120.040
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
5.	101.750	105.530	76.810	97.040	[illegible]	115.310	105.590	87.980	113.560	89.240	90.690	92.050	75.920	91.050	92.850
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	95.030	94.260	106.900	61.190	84.160	99.270	118.610	75.900	92.450	96.980	87.590	77.350	77.830	65.010	76.960
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	90.700	75.620	118.660	93.500	82.420	76.020	105.050	124.980	97.990	98.570	74.020	75.760	78.240	93.960	94.730
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	89.090	115.210	80.980	93.420	78.320	92.580	106.230	78.370	79.780	94.830	95.710	76.090	101.520	71.960	84.050
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	86.660	95.560	99.150	105.780	120.630	103.920	105.200	114.950	69.270	73.270	101.670	107.695	93.360	76.960	89.430
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	90.030	76.920	66.020	93.670	79.320	33.570	104.270	71.370	111.940	73.550	78.390	76.960	83.360	112.780	99.660
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	103.650	88.700	120.200	82.750	85.650	76.400	67.180	67.050	89.030	86.730	78.520	77.830	67.570	84.320	87.150
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	89.200	86.970	66.900	67.600	76.240	92.300	75.820	82.090	73.210	101.550	79.250	73.020	92.280	102.420	93.420
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	67.130	101.290	68.330	64.760	99.320	99.270	67.090	93.530	72.460	85.540	73.150	75.430	107.420	72.620	92.730
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	104.040	78.390	103.370	77.750	105.980	91.580	75.850	79.850	67.440	94.820	100.640	88.790	78.920	77.320	74.125
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	97.750	69.550	98.940	69.370	97.050	98.470	72.840	79.790	111.350	83.520	111.240	82.650	98.140	72.650	67.110

REPLICATION-2.

	16	29	46	59	76	89	106	119	136	149	166	179	196	209	226
1.	100.960	79.220	100.150	112.610	76.630	83.940	94.960	96.150	93.460	75.960	80.100	79.440	89.650	73.460	99.810
	1	18	31	46	61	76	91	106	121	136	151	166	181	196	211
2.	89.090	73.870	83.990	104.440	99.320	118.210	76.440	111.560	93.670	76.120	78.560	102.760	72.910	101.200	69.420
	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
3.	126.420	80.020	79.090	103.780	79.820	108.730	107.750	123.290	91.300	78.760	79.050	101.300	102.790	78.570	72.500
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	69.670	86.140	73.500	76.440	110.550	79.270	112.280	97.690	99.710	110.000	107.640	77.690	75.980	101.560	107.180
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	73.520	112.290	90.730	124.770	69.640	95.670	87.570	123.580	112.870	103.310	99.110	111.740	89.200	94.140	96.820
	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
6.	87.430	76.160	79.160	90.690	107.020	121.270	78.980	87.690	95.760	78.310	115.210	130.590	87.380	92.260	100.240
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	75.080	91.730	109.830	92.731	98.060	99.510	64.130	74.720	91.610	93.530	71.320	81.540	73.620	94.370	91.760
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	72.500	90.950	82.940	107.360	72.780	79.180	104.600	93.240	71.520	93.060	144.072	77.750	75.760	74.520	74.270
	5	16	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	71.190	120.950	76.590	78.740	102.280	121.900	93.540	79.180	122.730	76.930	109.190	107.060	99.510	125.120	99.920
	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
10.	87.920	115.350	103.690	91.990	101.890	93.040	78.810	72.830	83.090	115.540	100.870	104.530	99.630	109.730	99.710
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	103.330	101.710	72.750	73.550	68.350	93.420	72.390	63.330	76.590	76.460	91.520	93.690	88.160	90.380	70.970
	3	20	35	50	65	80	95	110	125	140	155	170	185	200	215
12.	89.540	113.760	77.280	80.360	98.960	117.650	87.120	92.270	94.500	93.020	89.140	111.230	112.620	94.920	103.970
	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214
13.	92.040	96.310	108.040	101.380	83.120	91.780	93.310	96.460	92.410	79.970	105.270	90.650	78.050	71.400	72.950
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	113.090	72.480	76.570	72.980	99.180	93.640	111.870	101.810	109.830	78.690	121.310	92.690	98.450	123.160	75.320
	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225
15.	81.870	102.660	79.090	115.920	86.930	75.190	98.690	93.690	77.710	95.920	92.660	91.090	81.680	121.160	89.180

REPLICATION-3.

	45	58	73	87	101	115	129	143	157	171	185	199	213	2	15
1.	94.270	110.450	113.470	90.550	81.070	79.010	125.260	91.020	122.140	94.060	87.240	76.550	91.020	74.240	75.200
	159	144	178	192	206	220	8	23	37	51	65	79	93	107	121
2.	105.380	80.040	109.000	98.450	99.910	110.090	129.090	83.160	89.590	104.850	100.060	105.240	124.120	113.520	123.580
	93	104	118	132	146	160	174	189	202	216	5	19	33	47	61
3.	78.150	96.690	74.020	87.140	81.010	78.020	113.330	74.425	93.720	97.190	98.690	100.420	78.690	78.110	90.660
	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166
4.	80.120	75.660	103.310	105.010	73.720	115.570	127.280	89.280	76.220	93.260	123.260	93.610	88.830	101.670	116.020
	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
5.	113.110	91.780	75.920	91.660	116.040	93.740	126.040	83.240	112.420	96.590	118.590	113.760	83.320	122.960	123.010
	180	194	208	222	11	25	39	53	67	81	95	109	123	137	151
6.	110.340	107.010	117.090	91.030	76.660	107.720	78.370	87.630	115.760	92.920	99.720	101.210	125.070	119.670	75.450
	68	76	89	102	116	130	144	158	172	186	200	214	3	17	31
7.	119.530	77.670	85.660	73.620	93.240	96.280	75.790	129.310	76.910	86.690	107.210	77.050	82.970	77.760	85.490
	75	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	90.910	77.960	104.010	96.240	108.390	105.150	109.130	120.960	117.250	106.240	124.720	105.640	127.030	96.020	98.590
	225	16	30	42	56	70	84	98	112	126	140	154	168	182	196
9.	99.010	129.240	123.730	85.970	117.070	119.390	101.800	116.780	118.920	128.490	96.630	124.600	104.580	79.920	83.960
	135	149	163	177	191	205	219	9	22	36	52	64	78	92	106
10.	79.010	76.010	108.160	99.560	91.060	106.050	96.260	78.150	78.310	129.230	85.100	106.600	123.170	82.070	113.090
	165	179	193	207	221	98	24	38	52	66	80	94	108	122	136
11.	81.900	79.290	101.260	112.760	97.110	82.240	79.460	94.840	78.160	83.510	125.060	103.260	79.160	120.730	92.090
	120	134	148	162	176	190	204	218	9	23	37	49	63	77	91
12.	97.830	100.650	126.290	91.170	125.940	75.990	89.240	93.060	121.230	113.960	88.760	106.270	120.020	101.200	75.310
	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1
13.	96.560	85.380	99.920	77.760	125.960	83.980	111.520	75.760	72.040	93.940	76.930	86.320	109.540	85.760	90.080
	75	89	103	117	131	145	159	173	187	201	215	4	18	32	46
14.	83.520	91.710	77.120	101.620	92.520	97.690	73.560	76.150	97.910	93.230	76.480	84.330	105.910	71.320	109.080
	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	94.810	93.880	98.980	115.230	79.300	101.230	81.320	81.760	120.690	110.270	93.750	88.280	96.720	81.370	81.170

APPENDIX VII Number of tillers per plant at Ellerslie

ELLERSLIE REPLICATION-1. NUMBER OF TILLERS PER PLANT

(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	12.300	9.700	10.600	10.500	12.000	9.700	9.700	12.500	10.400	12.500	11.200	9.800	10.600	10.500	10.500
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2.	10.700	9.800	15.400	11.400	12.300	9.200	8.300	9.700	10.200	10.700	8.200	11.900	12.100	9.400	12.300
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	9.600	10.333	11.300	12.000	8.700	10.300	12.300	8.200	9.400	8.300	11.200	8.500	11.100	11.000	9.300
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	10.400	12.000	11.800	10.300	11.900	10.900	9.700	7.400	11.000	7.400	8.500	9.200	10.100	8.600	12.600
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
5.	11.300	9.000	10.900	11.100	11.600	10.500	11.300	10.922	11.674	8.644	14.000	11.933	7.900	11.700	11.100
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	15.600	11.900	11.100	12.300	11.200	11.500	11.500	11.533	12.900	14.000	12.930	14.100	11.000	9.300	12.400
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	10.900	11.500	10.100	12.300	11.500	8.900	12.900	12.700	13.400	11.600	9.500	12.996	14.300	12.000	11.400
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	10.200	10.000	9.800	10.300	9.100	9.000	12.500	12.500	10.900	11.000	9.500	8.750	11.300	9.000	10.000
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	10.200	11.400	11.100	10.200	9.400	10.900	9.200	12.100	12.600	6.000	10.600	9.600	11.300	12.200	10.700
	1.	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	12.500	9.000	9.000	10.500	9.400	8.250	8.800	9.000	9.800	9.700	10.600	11.400	12.100	13.200	10.600
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	9.900	9.400	8.700	7.400	9.200	7.800	8.800	8.970	9.900	7.500	9.500	8.100	9.200	9.700	10.000
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	10.400	9.100	10.100	8.400	9.700	11.800	7.500	9.800	12.400	9.400	10.500	11.600	11.900	12.600	9.900
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	9.600	8.200	9.600	8.300	10.300	13.800	7.000	13.720	9.020	9.100	9.700	6.600	9.130	7.600	7.500
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	10.300	9.600	12.200	6.600	9.900	7.100	8.600	9.400	9.600	8.600	10.500	9.020	7.500	7.600	8.625
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	9.200	8.111	11.100	7.889	9.100	9.700	9.600	9.830	10.000	8.000	10.900	9.400	9.600	8.700	9.700

REPLICATION-2.

	16	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	10.900	9.700	9.100	11.000	10.000	9.500	10.200	9.620	12.200	11.600	12.200	11.900	12.000	8.800	12.100
	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
2.	11.600	12.900	15.222	9.600	11.600	15.700	8.700	9.900	11.000	9.600	12.000	10.400	10.111	12.600	11.667
	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
3.	15.100	12.600	12.700	11.000	11.100	13.4[illegible]	[illegible]	11.000	11.700	12.100	13.100	14.500	11.300	12.900	11.233
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	11.200	9.556	8.500	9.600	11.700	10.800	11.200	14.700	9.800	11.600	10.900	9.600	10.600	11.200	10.600
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	13.600	14.111	11.200	10.800	12.600	12.600	12.000	12.900	15.100	12.111	15.800	10.500	11.200	11.200	10.200
	17	25	41	56	71	86	101	116	131	146	161	176	191	206	221
6.	11.600	10.600	13.400	12.700	14.700	14.900	12.500	13.500	10.300	11.200	14.200	11.300	10.200	9.800	13.600
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	10.900	11.600	11.700	11.778	15.400	15.200	13.600	14.000	8.200	12.200	12.600	8.200	9.600	12.700	11.222
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	14.150	14.600	13.200	14.300	11.700	11.000	12.700	11.200	14.400	10.200	15.900	12.100	11.200	11.500	13.600
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	9.700	13.900	12.000	12.700	12.200	14.700	12.200	13.900	14.700	12.400	13.600	13.333	14.100	11.000	14.100
	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223
10.	12.900	12.600	15.000	9.100	11.600	12.500	10.600	9.700	11.600	11.800	11.900	10.900	13.600	14.300	10.900
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	13.300	9.300	13.600	9.600	8.800	11.600	11.600	11.600	12.100	11.100	9.220	9.900	8.100	14.700	11.700
	9	40	35	50	65	80	95	210	200	195	179	155	140	125	110
12.	9.700	14.900	9.600	11.820	11.600	13.700	14.100	15.200	12.600	14.770	10.200	11.100	11.120	10.600	11.020
	6	19	34	49	64	79	94	109	124	139	154	169	184	199	214
13.	11.300	12.200	14.100	11.700	11.100	8.600	15.520	10.700	7.400	11.600	11.900	9.600	9.700	8.500	11.020
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	14.300	11.200	10.600	12.700	12.333	11.900	12.200	11.120	15.600	11.300	11.700	11.200	14.020	11.700	13.100
	15	35	45	60	75	90	105	120	135	150	165	180	195	210	225
15.	15.700	10.100	11.100	10.600	12.200	10.700	10.200	10.000	11.900	9.900	10.020	11.300	9.900	14.600	8.100

REPLICATION-3.

	45	58	73	87	103	115	129	143	157	173	185	199	213	2	16
1.	9.700	11.600	12.600	12.900	11.920	11.600	11.100	12.500	10.700	12.300	11.100	11.500	10.200	11.600	10.100
	150	166	178	192	205	223	9	23	37	51	65	79	93	107	121
2.	12.330	14.500	10.120	12.400	11.333	13.700	11.600	14.100	12.600	14.660	11.200	11.500	11.600	13.200	14.900
	93	106	118	132	146	160	174	188	202	216	5	19	33	47	61
3.	12.200	13.600	10.100	15.900	13.600	8.300	12.200	11.600	9.900	10.600	11.100	9.600	11.600	12.000	9.600
	195	209	223	12	26	40	54	69	82	96	110	126	138	152	166
4.	12.900	12.600	13.700	11.600	11.976	11.100	15.100	12.111	12.700	15.600	14.732	13.700	14.600	10.500	10.100
	185	199	213	147	161	175	189	203	217	6	20	34	48	62	76
5.	15.600	12.100	12.600	13.100	12.700	12.300	13.700	15.100	11.200	14.500	13.500	14.600	11.600	14.500	15.500
	185	194	208	222	11	25	14	53	67	81	95	109	123	137	151
6.	14.330	11.500	14.300	11.300	10.200	13.600	12.300	12.200	11.600	12.000	10.900	12.700	14.900	12.400	9.000
	69	76	88	102	116	130	144	159	172	186	200	214	3	17	31
7.	15.500	14.900	11.930	12.900	13.400	14.800	12.800	12.700	13.500	13.300	13.700	13.500	11.700	12.200	11.111
	35	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	13.400	14.600	17.500	13.700	14.200	13.700	14.900	15.700	12.600	15.200	15.970	14.100	15.220	13.600	9.200
	225	14	28	43	56	70	84	98	112	126	140	154	168	182	196
9.	14.150	14.700	13.600	15.100	12.900	13.100	15.100	11.200	13.500	15.300	13.176	11.300	9.700	12.500	14.200
	535	149	163	177	191	205	219	8	22	36	50	64	78	92	106
10.	14.230	12.700	12.300	14.900	14.330	14.500	13.300	14.900	15.566	13.100	15.000	9.600	15.200	14.200	15.600
	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136
11.	11.200	9.100	12.600	14.700	11.700	10.500	14.700	13.400	11.120	15.500	13.500	15.500	13.600	11.800	14.700
	128	134	148	162	176	190	204	218	7	21	35	49	63	77	91
12.	10.900	13.100	12.500	12.200	11.600	9.300	10.100	10.500	10.100	9.700	12.600	12.600	9.000	14.100	10.600
	33	48	58	72	86	100	114	128	142	156	170	184	198	212	8
13.	14.550	10.770	13.100	11.500	12.700	11.600	12.600	11.120	10.600	12.000	9.600	11.300	13.600	12.000	15.000
	75	83	103	117	131	145	159	173	187	201	215	6	10	32	46
14.	11.600	13.600	13.600	13.600	12.100	11.500	12.930	11.300	9.900	11.600	11.200	11.900	10.500	7.500	12.900
	216	224	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	11.500	12.600	9.000	12.600	11.300	11.000	12.200	9.700	12.600	10.000	10.200	9.600	12.700	13.100	10.600

APPENDIX VIII Number of spikelets per spike at Ellerslie

ELLERSLIE APPLICATION 1. NUMBER OF SPIKELETS PER SPIKE

Block	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115
1.	18.333	13.000	14.333	15.100	13.700	14.900	15.433	13.100	14.733	12.933	14.300	13.967	14.367	13.733	14.433
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2.	11.667	13.100	14.000	13.667	12.033	14.933	12.967	12.200	12.667	13.567	14.667	15.133	14.167	14.033	14.267
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	13.333	13.467	13.933	13.567	13.633	12.400	14.967	14.233	14.267	15.133	13.267	14.567	13.733	14.733	13.733
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	14.533	13.333	13.633	14.133	14.367	15.100	15.800	14.200	15.233	13.500	14.667	14.600	15.533	15.567	14.667
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
5.	14.300	14.567	13.733	14.550	15.467	14.767	14.633	13.975	15.313	12.965	13.300	13.933	13.900	13.267	13.350
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	14.667	15.933	15.733	13.133	14.567	14.767	15.767	14.967	16.833	15.767	15.133	14.733	15.467	13.833	14.350
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	14.733	12.833	14.667	15.733	13.600	15.133	14.633	14.033	17.633	15.133	12.600	14.133	15.133	13.267	14.967
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	14.600	15.933	14.833	15.900	14.367	12.600	15.200	14.500	11.783	14.667	16.667	14.200	15.133	13.500	14.567
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	12.667	13.733	15.000	15.333	15.133	16.633	15.600	15.767	14.133	17.933	16.633	15.233	16.333	13.133	15.200
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	13.300	12.700	15.600	14.267	12.600	14.200	14.633	14.167	14.650	11.875	13.467	15.500	14.867	17.833	12.367
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	12.567	13.633	14.433	11.367	15.467	12.367	11.033	13.833	12.167	12.100	12.733	12.900	14.467	13.133	12.500
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	13.167	13.267	11.500	13.100	11.750	14.233	13.500	12.767	14.300	14.367	12.833	13.933	12.733	15.800	15.400
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	13.300	15.633	13.467	13.467	14.000	13.633	12.967	17.567	13.067	12.933	13.500	13.267	14.533	13.767	13.967
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	15.167	13.567	14.200	13.533	14.633	13.067	14.233	12.567	14.933	13.567	15.700	15.633	14.100	13.967	14.250
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	15.100	11.767	14.500	12.533	12.567	14.667	13.933	14.333	14.933	12.600	15.200	12.933	15.633	13.533	13.733

REPLICATION-2.

	16	29	44	59	74	89	104	119	134	149	164	179	194	209	224
1.	15.733	13.750	14.567	13.633	13.667	15.667	14.633	13.933	15.000	13.952	12.567	12.967	12.933	15.833	15.033
	9	16	31	46	61	76	91	106	121	136	151	166	181	196	211
2.	12.967	13.633	14.296	12.633	13.140	14.000	14.350	14.633	15.133	12.333	12.000	14.167	11.593	12.733	14.017
	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219
3.	15.600	12.167	12.733	14.333	13.167	14.933	14.667	15.933	14.583	14.533	12.833	15.100	12.933	12.733	14.067
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	12.833	13.661	12.867	12.633	15.200	12.815	12.667	13.500	13.067	15.200	14.567	11.233	13.067	14.733	14.767
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	12.633	15.630	15.133	15.767	12.633	13.833	15.267	14.600	15.200	12.925	13.967	14.300	14.240	13.667	15.503
	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
6.	13.733	13.600	12.133	15.333	14.633	14.633	12.833	13.033	13.133	12.933	14.467	14.367	12.500	12.700	14.267
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	12.500	13.967	15.300	13.466	13.267	14.633	13.367	13.633	12.633	13.500	12.160	12.833	13.067	15.833	14.706
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	13.067	13.900	12.000	15.133	13.296	12.633	14.600	13.533	13.833	14.400	15.220	12.267	13.167	13.900	14.233
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	14.233	14.733	13.067	12.067	13.633	14.933	15.067	15.200	15.067	13.133	12.933	14.100	12.733	14.267	15.267
	33	28	43	58	73	88	103	118	133	148	163	178	193	208	223
10.	13.733	14.267	13.267	13.766	15.600	15.067	12.200	13.667	12.967	14.233	15.967	12.600	13.133	15.267	14.733
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	14.733	15.267	14.067	13.933	13.700	14.833	13.867	14.233	15.033	14.333	14.300	13.633	13.200	13.733	14.633
	5	20	35	50	65	80	95	210	220	185	170	155	140	125	110
12.	15.033	14.333	12.933	14.967	14.933	14.700	14.267	14.067	13.600	15.550	14.333	14.367	14.233	13.833	14.533
	6	19	34	49	64	79	94	109	124	139	154	169	184	199	214
13.	15.833	15.300	11.267	13.967	14.100	14.867	15.567	14.633	14.100	15.683	15.726	15.733	12.967	13.533	13.933
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	15.933	14.967	14.500	13.296	15.611	12.933	12.633	15.267	14.767	14.000	17.133	13.630	14.133	13.238	14.267
	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225
15.	13.967	12.700	13.967	14.233	14.267	14.900	14.167	14.733	13.933	13.600	14.267	15.967	13.633	15.300	14.967

REPLICATION-3.

	93	58	73	87	103	118	129	143	157	171	185	199	213	2	16
1.	13.933	14.733	15.300	15.267	14.967	13.633	14.170	13.633	14.167	13.567	13.467	14.600	13.667	14.867	13.267
	150	164	179	192	206	223	9	23	37	51	65	79	91	107	121
2.	14.267	14.333	13.733	14.133	15.233	15.433	14.667	14.350	15.233	15.500	14.533	15.533	14.033	14.967	15.767
	88	104	118	132	146	160	174	189	202	216	4	19	33	47	61
3.	14.767	14.933	14.436	12.900	13.767	12.900	15.133	13.492	13.167	13.900	15.267	12.700	12.211	13.500	15.100
	195	209	223	12	26	40	56	69	82	95	110	124	138	152	166
4.	12.900	14.900	14.000	13.900	13.310	14.600	14.733	14.594	14.900	14.100	14.467	14.133	15.633	14.533	13.020
	105	119	133	147	161	175	189	203	217	6	20	34	48	62	76
5.	14.267	15.367	13.067	14.633	14.967	13.367	15.133	14.267	14.233	14.267	15.767	13.833	13.767	15.667	15.833
	100	114	209	222	11	25	31	53	67	81	95	109	123	137	151
6.	15.500	13.600	14.600	14.033	13.900	14.233	13.767	13.500	14.067	14.700	14.567	14.500	15.667	15.233	12.300
	60	76	90	102	116	130	144	158	172	186	200	214	3	17	31
7.	14.900	14.633	15.900	14.600	14.302	15.630	14.533	12.367	15.767	15.100	14.233	14.233	14.733	15.767	14.111
	55	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	15.367	15.667	14.767	15.767	14.867	15.967	15.967	15.420	15.000	14.933	14.600	15.433	14.767	13.833	14.667
	225	16	28	42	56	70	85	99	112	126	140	154	168	182	196
9.	15.667	13.700	14.700	14.767	14.767	14.100	15.633	14.767	15.733	14.933	14.933	12.300	13.867	15.667	14.367
	135	149	163	177	191	205	219	8	22	36	50	64	78	92	106
10.	14.833	13.633	15.267	14.200	15.167	15.633	14.367	13.033	15.267	14.267	14.633	14.700	14.600	14.967	13.700
	165	179	193	207	221	19	34	48	52	66	80	94	108	120	134
11.	15.833	13.567	15.600	15.467	14.700	13.900	14.933	14.933	14.933	14.600	14.133	14.967	14.533	14.867	14.667
	120	136	148	162	176	190	204	218	7	21	35	49	63	77	91
12.	15.867	13.667	17.533	14.200	13.167	12.167	14.767	13.967	13.867	14.200	13.100	15.533	14.200	14.933	13.600
	38	53	68	83	96	108	119	134	142	156	170	184	198	212	1
13.	14.933	13.667	14.300	14.633	14.833	13.667	14.267	15.167	13.500	15.267	13.533	12.433	13.667	15.800	15.833
	75	89	103	117	131	145	159	173	187	201	215	9	18	32	46
14.	14.200	14.233	13.533	15.967	14.167	14.900	14.700	15.200	14.033	15.567	13.667	14.767	13.267	13.867	13.633
	210	220	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	14.000	14.967	13.767	17.100	14.767	14.167	14.267	14.833	14.400	15.233	15.267	14.633	14.533	14.233	15.267

APPENDIX IX Number of seeds per spike at Ellerslie

REPLICATE REPLICATION-1. NUMBER OF SEEDS PER SPIKE

(Block)																
1.	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	
	55.667	49.833	44.667	57.433	49.067	47.333	49.833	36.967	48.600	48.700	44.667	51.733	42.198	49.500	57.367	
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
	48.233	49.867	49.333	49.733	48.767	48.067	57.633	43.903	44.600	49.233	58.400	42.067	48.600	49.000	48.933	
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	
	52.967	38.815	52.667	43.833	47.867	50.200	59.633	43.100	44.333	52.067	39.600	45.333	43.167	43.333	58.867	
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
	48.520	39.500	38.667	38.700	42.367	48.067	47.067	43.200	47.633	48.900	56.600	48.367	58.933	45.000	53.733	
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	
	49.267	43.667	43.100	58.767	53.933	54.667	42.870	46.200	44.134	47.766	42.633	49.733	44.867	50.300	45.030	
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	
	56.667	58.033	49.767	43.500	53.867	51.233	43.267	45.433	52.900	48.133	47.140	38.800	58.767	42.700	43.767	
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	
	58.867	47.533	52.867	52.967	46.933	53.900	48.867	44.403	51.533	43.933	48.567	46.367	46.400	44.167	45.200	
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	
	44.133	58.667	49.833	61.700	46.833	49.267	58.567	48.633	37.900	49.500	54.333	45.267	52.167	42.700	56.100	
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	
	47.733	47.700	47.133	58.900	49.333	55.933	47.000	52.833	43.867	43.733	58.900	52.633	42.700	45.033	44.933	
10.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
	45.833	52.833	58.033	54.033	45.833	48.200	42.800	45.233	56.233	38.633	43.200	58.233	36.333	55.967	41.633	
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	
	42.833	48.100	57.667	48.333	48.400	52.067	42.733	45.533	58.967	45.067	47.767	42.533	49.133	46.267	43.667	
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
	43.133	58.433	39.067	38.900	49.300	58.133	45.833	46.267	49.000	48.933	39.500	42.467	42.133	47.133	41.000	
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	
	40.567	53.567	48.833	47.233	52.400	42.933	41.100	56.767	39.233	48.900	46.200	58.067	46.067	42.511	53.767	
14.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	
	43.000	36.600	58.033	42.500	45.133	44.067	37.900	39.867	48.167	42.667	47.700	51.967	45.900	47.433	49.917	
15.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	
	54.833	36.978	43.533	39.889	43.367	46.533	46.767	46.867	50.500	36.533	47.400	47.700	41.167	43.867	48.700	

REPLICATION-2.

1.	76	29	30	31	32	33	34	35	36	37	38	39	40	41	42	
	51.733	53.433	45.267	44.567	46.867	41.733	49.067	49.333	53.700	48.378	44.111	42.267	46.533	59.967	48.700	
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211	
	46.533	49.700	48.733	48.900	43.733	51.000	56.300	51.067	56.033	46.100	44.333	46.333	39.967	42.467	45.767	
3.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219	
	58.133	39.667	42.200	49.467	47.333	50.667	50.700	46.833	50.100	38.100	44.333	47.567	47.667	44.333	49.944	
4.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212	
	51.233	50.889	53.433	38.867	53.067	52.867	43.533	40.300	47.867	47.367	39.700	38.000	49.833	45.967	45.967	
5.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216	
	52.667	57.333	52.167	48.267	46.867	51.433	53.767	53.767	48.567	42.533	48.833	46.933	46.533	48.300	57.633	
6.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221	
	49.867	38.233	37.300	58.167	46.733	46.067	43.200	37.600	48.133	44.633	50.267	48.733	31.333	53.967	42.667	
7.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220	
	38.233	49.667	53.500	46.700	45.000	42.500	48.233	47.733	38.700	44.067	48.333	47.100	50.633	46.033	54.767	
8.	4	21	38	53	68	83	98	113	128	143	158	173	188	203	218	
	47.833	42.500	37.067	53.300	43.533	44.267	56.200	49.067	55.233	52.567	46.667	46.167	41.300	46.500	44.367	
9.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213	
	59.233	43.933	41.733	36.467	46.700	45.167	44.667	36.933	51.033	46.733	42.700	46.733	49.833	37.467	52.733	
10.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223	
	38.533	47.500	45.667	46.733	46.267	45.800	42.867	46.167	38.633	51.067	43.167	41.833	43.667	59.667	47.167	
11.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222	
	53.833	41.367	43.667	53.300	45.767	53.167	44.200	46.367	43.933	48.500	42.767	44.983	43.133	42.500	44.633	
12.	5	20	35	50	65	80	95	215	230	245	170	185	200	125	140	
	49.767	49.867	34.567	47.167	45.867	53.867	43.633	49.833	50.733	56.370	44.333	46.833	45.367	44.967	43.133	
13.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218	
	49.100	45.167	45.667	47.267	52.967	47.533	47.633	37.933	45.167	47.333	51.222	49.200	41.567	43.233	49.833	
14.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217	
	48.900	46.733	50.800	41.259	48.356	41.933	41.867	48.200	59.367	44.926	49.960	42.267	41.533	56.000	46.833	
15.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225	
	45.300	48.333	49.967	38.930	55.867	46.267	42.900	46.933	37.033	45.967	43.958	47.933	48.767	39.167	43.167	

REPLICATION-3.

1.	55	58	73	87	101	115	129	143	157	171	185	199	213	2	16	
	46.467	42.833	49.100	48.867	49.867	46.533	54.867	47.867	47.900	43.600	43.467	53.033	48.367	44.000	43.500	
2.	153	168	178	192	206	220	9	23	37	51	65	79	93	107	121	
	42.200	38.400	43.200	51.767	53.933	55.233	48.933	42.267	58.133	56.033	49.967	45.733	49.800	44.867	48.333	
3.	98	124	138	152	166	180	194	208	222	236	5	19	33	47	61	
	56.967	55.400	57.533	48.367	51.767	46.533	44.967	45.000	48.733	52.267	54.767	41.133	44.933	46.100	47.367	
4.	155	269	223	32	46	48	54	58	62	96	110	124	138	152	166	
	47.100	54.433	46.500	47.167	49.766	46.133	50.400	46.342	48.533	44.200	48.542	49.567	52.633	46.000	41.700	
5.	135	119	133	147	161	175	189	203	217	6	20	34	48	62	76	
	42.767	53.600	49.100	48.267	48.733	43.900	51.333	41.233	48.933	46.967	48.067	47.267	48.300	52.233	52.367	
6.	188	194	208	222	11	25	39	53	67	81	95	109	123	137	151	
	51.583	42.033	45.367	46.233	47.233	45.833	49.133	38.033	51.967	49.200	48.967	46.750	43.750	50.133	45.133	
7.	68	74	88	102	116	130	144	158	172	186	200	214	3	17	31	
	50.567	42.067	55.233	47.967	52.200	46.733	41.000	37.267	51.667	51.900	44.633	48.667	48.267	48.067	49.467	
8.	95	29	43	57	71	85	99	113	127	141	155	169	183	197	211	
	50.067	47.733	42.533	50.167	50.967	42.933	49.933	46.233	50.567	43.200	47.100	45.567	41.933	42.900	52.033	
9.	225	16	20	42	56	70	84	98	112	126	140	154	168	182	196	
	53.867	43.667	49.067	41.400	56.433	45.867	48.800	47.667	44.800	52.533	54.281	44.667	48.856	48.833	50.967	
10.	125	149	163	177	191	205	219	8	22	35	50	64	78	92	106	
	48.367	39.733	44.233	46.967	46.200	47.467	43.467	45.233	48.500	48.167	43.267	45.033	50.033	45.333	54.189	
11.	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136	
	51.900	43.200	53.500	45.167	48.900	39.233	46.867	48.700	51.233	49.467	45.400	48.067	42.867	52.133	47.967	
12.	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91	
	51.867	46.900	51.533	46.750	48.633	52.167	56.400	43.500	43.100	43.700	33.967	41.800	43.300	43.633	41.867	
13.	38	60	58	73	86	100	114	128	142	156	170	184	198	212	9	
	49.633	48.000	45.900	43.500	47.000	49.267	46.233	48.567	43.600	48.267	41.200	42.633	43.833	36.700	45.900	
14.	75	89	103	117	131	145	159	173	187	201	215	6	35	32	46	
	51.233	46.167	39.867	51.200	51.967	43.733	55.667	49.433	43.733	48.833	43.133	49.633	46.767	47.900	45.600	
15.	210	224	12	27	41	55	69	83	97	111	125	139	153	167	181	
	45.533	46.833	48.867	46.567	46.700	45.267	45.300	47.067	47.200	43.500	53.733	50.667	41.933	48.333	47.533	

APPENDIX X Weight of seeds per spike at Ellerslie

REPLICATION-I. WEIGHT OF SEEDS PER SPIKE

(Blocks)															
	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	3.977	2.681	3.656	2.617	3.046	2.385	2.838	3.665	2.347	3.760	3.011	3.701	3.685	3.731	2.359
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2.	3.596	3.043	3.775	3.365	3.025	2.913	2.256	3.466	3.958	3.048	4.320	3.515	3.731	2.053	3.559
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	3.544	3.446	3.050	3.468	2.583	3.022	3.351	3.789	3.766	2.018	3.673	2.694	3.765	3.578	3.748
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	3.967	3.837	3.752	3.618	3.981	3.944	2.811	3.580	3.784	3.598	2.358	3.937	3.873	3.468	3.854
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
5.	3.776	3.256	3.785	3.646	3.097	3.888	3.926	3.854	3.513	3.944	3.958	3.819	3.758	3.880	3.683
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	3.888	3.743	3.453	3.143	3.907	3.828	2.216	3.666	3.885	3.522	3.688	3.627	2.932	3.535	3.742
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	3.267	3.983	3.867	3.812	3.993	3.344	3.332	3.819	3.899	3.929	3.998	3.512	3.818	3.822	3.632
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	3.606	3.796	3.934	2.329	3.628	3.887	3.905	3.897	3.665	3.963	3.735	3.938	3.869	3.457	2.260
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	3.753	3.697	3.561	3.523	3.668	3.785	3.511	3.618	3.877	3.561	3.954	3.937	3.365	3.561	3.879
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	3.567	3.923	2.227	3.991	3.748	3.993	3.615	3.664	3.767	3.359	3.669	3.716	3.307	3.676	3.513
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	3.617	3.461	3.795	3.635	3.522	3.634	3.563	3.749	3.910	3.524	3.794	3.695	3.556	3.649	3.339
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	3.656	3.988	3.576	3.358	3.554	3.705	3.836	3.749	3.384	3.578	3.523	3.665	3.435	3.628	2.317
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	3.687	3.613	3.976	3.313	3.892	3.727	3.666	2.295	3.428	3.965	3.654	3.945	3.513	3.761	3.678
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	3.283	3.358	3.685	3.822	3.534	3.536	3.353	3.613	3.573	3.567	3.464	3.757	3.688	3.764	2.223
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	3.953	3.325	3.699	3.559	3.692	3.693	3.673	3.873	3.602	3.373	3.537	3.632	3.467	3.804	3.673

REPLICATION-II.

	31	29	28	59	76	95	126	119	136	149	160	179	198	209	220
1.	3.689	3.955	4.553	3.576	3.899	2.375	3.876	3.633	3.134	3.357	3.876	3.760	3.566	2.494	3.760
	9	10	31	46	61	76	91	106	121	136	151	166	181	196	211
2.	3.633	3.926	3.685	3.698	3.695	3.926	2.361	3.786	2.172	3.670	2.933	2.331	3.679	3.625	3.725
	9	24	29	54	69	84	99	114	129	144	159	174	189	204	219
3.	3.999	3.578	3.627	3.769	3.803	2.110	2.496	3.670	2.028	3.676	3.933	3.739	2.695	3.984	3.862
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	3.872	2.339	2.099	3.625	3.629	3.193	3.692	3.378	3.727	3.756	3.659	3.645	3.885	3.540	3.676
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	3.962	3.864	3.873	3.617	3.894	3.731	2.362	3.843	3.865	3.584	3.671	3.875	3.801	3.763	2.431
	23	24	41	56	71	86	101	116	131	146	161	176	191	206	221
6.	2.783	3.533	3.547	2.128	3.676	3.611	3.453	3.824	3.667	3.648	3.739	3.563	3.204	2.044	3.394
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	3.341	3.634	3.391	3.661	3.667	3.636	3.432	2.806	3.568	3.926	2.387	3.582	3.661	3.754	2.675
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	2.831	3.765	3.673	3.819	3.846	3.878	3.852	3.812	2.198	3.974	3.520	3.699	3.723	3.822	3.758
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	2.337	3.674	3.749	3.623	3.832	3.506	3.564	3.464	3.219	3.624	3.625	3.913	3.497	3.807	3.823
	33	28	43	58	73	88	103	118	133	148	163	178	193	208	223
10.	3.467	3.572	3.265	3.563	3.589	3.545	3.443	3.880	3.875	3.656	3.633	3.658	3.575	3.825	3.732
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	3.732	3.672	3.639	3.887	3.893	3.707	3.868	3.654	3.573	3.650	3.504	3.639	3.678	3.537	3.728
	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
12.	3.855	3.622	3.285	3.539	3.779	3.826	3.603	3.275	3.798	3.069	3.526	3.569	3.661	3.701	3.903
	6	21	36	49	64	79	94	109	124	139	154	169	184	199	214
13.	3.918	3.931	3.648	3.723	3.868	3.733	3.540	3.938	3.560	3.816	3.378	3.619	3.519	3.582	3.833
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	3.519	3.602	3.933	3.626	3.208	3.511	3.619	3.656	2.316	3.704	3.564	3.731	3.755	3.922	3.783
	35	30	45	60	75	90	105	120	135	150	165	180	195	210	225
15.	3.666	3.934	3.859	3.966	3.385	3.683	3.331	3.662	3.661	3.815	3.339	3.576	3.538	3.618	3.333

REPLICATION-III.

	31	29	28	59	76	95	126	119	136	149	160	179	198	209	220
1.	3.689	3.955	4.553	3.576	3.899	2.375	3.876	3.633	3.134	3.357	3.876	3.760	3.566	2.494	3.760
	110	144	170	192	208	220	0	23	37	53	65	79	91	107	121
2.	3.644	2.875	3.726	3.945	2.250	2.618	3.660	3.869	2.676	2.278	2.720	3.614	3.892	3.935	2.910
	93	104	119	132	146	160	176	190	202	216	5	19	33	47	61
3.	2.267	2.267	2.653	3.589	2.389	2.192	3.792	2.069	3.991	2.260	2.509	3.693	3.895	3.869	3.615
	205	209	223	12	26	43	56	68	82	96	110	123	138	152	166
4.	3.765	2.218	3.029	3.550	3.928	3.721	3.697	3.729	2.155	3.734	3.581	3.932	2.147	3.836	3.612
	185	219	233	247	261	275	290	233	317	6	20	36	48	62	76
5.	3.369	2.606	3.730	3.613	3.755	3.583	3.659	3.606	3.812	3.963	3.725	3.525	3.802	3.750	3.783
	189	199	200	222	11	25	39	53	67	81	95	109	123	137	151
6.	3.792	3.963	3.658	3.670	3.789	3.390	3.849	3.186	3.927	3.695	3.668	3.573	3.781	3.909	3.617
	80	36	48	102	116	130	144	159	172	186	200	214	3	17	31
7.	3.575	3.920	2.263	3.869	3.522	3.569	3.789	3.551	2.013	2.210	3.506	3.581	3.911	3.729	3.756
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	3.922	3.779	3.364	3.268	3.865	3.677	3.796	3.669	3.776	3.636	3.659	3.660	3.698	3.655	2.239
	225	34	28	42	56	70	84	98	112	126	140	156	168	182	196
9.	2.112	3.639	3.876	3.659	2.102	3.733	3.747	3.759	3.692	3.738	3.687	3.695	3.695	2.073	2.108
	135	149	163	177	191	205	219	6	22	36	50	64	78	92	106
10.	3.960	3.978	3.575	3.968	3.733	3.976	3.823	3.905	3.915	3.693	3.842	3.621	3.715	3.811	3.618
	105	119	133	207	221	10	24	38	52	66	80	94	110	122	136
11.	2.039	3.606	3.602	3.823	3.606	3.182	3.893	3.851	2.086	3.977	3.995	3.831	2.026	2.090	3.737
	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91
12.	3.571	3.918	3.781	3.589	3.731	3.852	2.102	3.926	3.557	3.697	3.330	3.701	3.709	3.570	3.633
	30	44	59	72	86	100	114	128	142	156	170	184	198	212	0
13.	3.827	3.749	3.616	3.838	3.688	3.666	3.683	3.766	3.632	3.760	3.563	3.563	2.006	3.368	3.609
	75	88	103	117	131	145	159	173	187	201	215	0	16	32	46
14.	3.858	3.972	3.369	3.758	3.998	3.969	2.075	3.971	3.739	3.815	3.834	3.811	3.563	3.667	3.758
	250	226	13	27	45	55	69	83	97	111	125	139	153	167	181
15.	3.883	3.838	3.628	3.958	3.818	3.883	3.855	3.998	3.516	3.892	3.803	3.996	3.678	3.529	3.988

APPENDIX XI 1000-kernel weight at Ellerslie

ELLERSLIE REPLICATION-1. 1000-KERNEL-WEIGHT

(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	40.360	41.059	37.309	41.911	43.067	43.240	40.671	40.560	43.958	42.656	40.306	39.426	37.353	38.772	41.058
	15	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2.	38.621	42.099	36.068	35.462	40.359	35.046	39.388	42.262	44.011	39.591	45.723	36.027	36.547	41.869	38.987
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	38.234	42.769	35.401	42.469	43.083	43.444	36.551	41.438	42.627	38.126	37.506	42.367	39.020	35.823	34.397
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	39.967	45.895	46.977	36.727	44.716	38.099	42.693	36.296	37.196	39.500	41.498	40.029	37.638	32.670	38.905
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
5.	35.851	38.914	39.621	31.151	35.203	34.645	33.451	35.468	31.545	40.859	36.472	36.147	41.566	37.736	35.676
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	33.293	37.973	29.234	27.647	37.530	35.193	35.082	41.618	37.764	38.369	35.187	37.793	42.036	35.998	39.958
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	40.206	41.811	35.516	35.262	42.623	43.209	32.709	36.797	36.829	39.844	40.738	41.101	41.093	38.432	34.869
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	43.707	35.288	36.536	34.209	33.534	37.713	32.543	38.159	38.607	33.443	32.077	39.261	35.671	38.696	40.288
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	37.225	35.588	33.632	41.732	38.178	32.389	32.163	38.567	37.523	35.624	33.634	38.265	32.230	34.877	39.857
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	36.619	36.435	39.678	36.663	37.596	38.692	32.906	44.171	38.329	35.683	36.768	36.145	37.987	32.287	35.952
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	37.791	36.667	38.489	36.261	38.283	38.187	36.706	37.939	39.365	33.674	38.106	35.273	35.353	36.649	38.004
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	36.763	37.389	42.478	38.662	37.368	38.546	40.262	35.065	39.373	32.761	39.343	37.867	36.190	35.179	33.473
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	36.427	35.646	41.039	37.772	37.670	40.125	39.376	43.067	41.679	35.985	40.001	36.491	36.238	40.914	36.836
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	29.728	33.361	33.193	37.671	33.709	36.387	36.188	40.648	35.949	37.251	30.722	33.613	37.217	37.359	40.220
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	35.083	34.169	36.725	39.672	36.929	38.935	44.283	42.877	33.622	37.625	31.797	35.676	35.288	36.965	35.685

REPLICATION-2.

	16	29	44	59	76	93	106	119	134	149	164	179	194	209	224
1.	32.284	38.505	34.789	35.564	36.814	37.283	37.997	33.283	30.125	40.424	40.373	41.366	33.851	41.695	36.292
	1	14	31	46	61	76	91	106	121	136	151	166	181	196	211
2.	36.727	38.581	32.691	34.336	39.051	36.649	42.229	35.675	38.103	43.665	50.193	35.568	42.379	38.214	37.528
	9	21	39	56	69	84	99	114	129	144	159	174	189	204	219
3.	33.977	39.813	38.674	35.065	43.627	42.469	41.236	37.691	40.047	44.576	44.828	36.187	43.020	40.047	37.354
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	36.423	42.223	41.671	41.861	32.766	33.179	38.371	39.224	35.351	36.323	36.561	39.771	37.934	33.633	35.636
	6	23	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	34.367	32.903	36.781	37.913	40.421	34.713	40.159	38.662	34.316	35.915	38.971	39.408	37.044	36.659	43.620
	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
6.	42.523	39.595	43.618	36.778	39.692	35.604	42.450	38.277	39.199	37.905	31.956	32.016	38.619	40.427	33.784
	13	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	33.769	33.693	37.845	35.451	37.886	43.260	35.606	42.724	39.640	41.043	43.365	42.157	36.880	38.012	37.808
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	42.278	43.983	39.247	35.029	37.206	35.918	31.935	37.483	39.511	37.599	32.615	35.418	41.635	40.595	39.511
	5	18	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	39.326	38.965	41.476	44.358	39.269	37.275	35.027	38.552	33.442	36.776	38.395	39.353	38.679	39.754	36.934
	12	29	43	58	73	88	103	118	133	148	163	178	193	208	223
10.	38.758	33.628	36.510	35.964	35.903	33.029	33.693	39.439	39.259	32.624	33.051	42.114	33.042	35.593	38.392
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	32.646	36.163	37.506	38.381	41.588	35.683	42.493	35.614	36.252	36.252	34.730	35.658	38.527	37.115	35.393
	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
12.	36.963	32.326	34.294	36.210	38.883	35.622	36.858	46.992	35.556	36.751	34.569	38.456	36.964	37.652	33.602
	8	19	34	49	64	79	94	109	124	139	154	169	184	199	214
13.	39.716	35.767	36.129	36.152	37.776	35.478	32.771	38.776	36.263	43.815	35.817	36.399	36.186	37.712	38.746
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	31.088	36.151	37.607	39.296	25.179	36.658	38.143	38.389	36.232	38.478	33.551	40.122	42.372	36.765	38.973
	15	32	45	60	75	90	105	120	135	150	165	180	195	210	225
15.	33.739	35.943	37.224	37.675	38.227	36.652	38.972	32.865	39.096	40.050	31.125	31.681	36.261	35.954	38.447

REPLICATION-3.

	45	58	73	87	101	115	129	143	157	171	185	199	213	2	16
1.	37.928	39.459	39.642	36.730	46.229	43.598	36.781	36.751	37.665	36.789	36.367	41.258	39.273	39.094	38.756
	153	154	170	182	206	220	8	23	37	51	65	75	91	107	121
2.	38.951	41.211	40.331	35.077	42.043	36.594	33.534	40.577	46.603	38.693	42.328	36.315	37.696	41.736	40.329
	93	105	119	132	146	160	174	188	202	216	5	19	33	47	61
3.	35.669	46.537	46.142	35.798	46.236	44.178	37.265	45.933	43.180	43.978	47.169	36.328	44.992	36.836	35.522
	195	209	223	12	25	42	56	69	87	96	110	124	138	152	166
4.	36.651	40.783	39.504	39.005	42.237	39.191	33.628	38.056	44.671	39.085	37.631	39.244	41.218	37.205	38.022
	125	139	153	167	181	195	209	223	237	6	20	34	48	62	76
5.	32.106	37.668	35.092	43.187	37.732	36.146	36.180	39.169	39.191	41.932	35.830	35.131	38.213	39.106	33.067
	183	196	220	232	11	25	39	53	67	81	95	109	123	137	151
6.	35.977	35.688	36.530	42.912	37.550	35.153	33.321	35.965	33.679	36.629	35.347	37.249	35.346	35.727	36.949
	63	76	90	102	116	130	144	158	172	186	200	214	3	17	31
7.	31.545	35.269	40.937	39.392	35.542	35.093	38.381	41.304	39.968	39.069	38.993	35.258	38.320	35.958	35.331
	95	29	43	57	31	95	99	133	127	161	155	169	183	197	211
8.	34.326	37.197	31.559	44.896	37.226	39.241	35.737	38.572	35.185	37.957	36.503	37.381	35.817	38.342	33.619
	225	16	28	42	56	73	86	98	112	126	140	154	168	182	196
9.	38.169	37.976	36.282	43.237	38.542	38.107	38.123	38.816	32.455	32.896	38.338	38.604	35.362	42.046	33.679
	135	149	163	177	191	205	219	6	22	36	50	64	78	92	106
10.	40.227	39.367	35.606	36.836	39.293	41.948	43.655	41.897	39.368	39.166	43.304	36.031	35.286	39.571	39.448
	165	179	193	207	221	10	24	38	52	66	81	96	108	122	136
11.	39.216	39.013	35.228	35.836	36.515	39.564	39.932	39.909	40.088	40.066	32.601	33.100	43.981	39.322	35.883
	120	130	148	162	176	192	206	218	7	21	35	49	63	77	91
12.	32.878	32.568	36.448	37.157	39.149	36.016	38.795	36.965	36.020	38.677	39.723	43.439	40.853	37.619	39.500
	33	46	58	72	85	103	116	128	142	156	170	186	198	212	1
13.	35.908	37.198	35.708	42.378	38.006	35.089	38.378	36.616	41.231	36.368	37.815	37.078	32.923	36.598	35.196
	75	89	103	117	131	145	159	173	187	201	215	8	18	32	46
14.	36.125	34.115	34.967	33.935	38.548	35.236	36.686	40.182	39.056	37.117	42.524	34.105	35.027	35.719	36.185
	213	226	13	27	41	55	69	83	97	111	125	139	153	167	181
15.	38.617	39.525	34.643	35.456	36.993	32.297	33.980	43.769	31.914	35.093	36.467	39.293	38.778	38.319	37.835

APPENDIX XII Yield per plant at Ellerslie

ELLERSLIE REPLICATION-1. YIELD PER PLANT

(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	20.016	13.998	16.198	22.956	21.632	17.581	13.546	13.670	16.172	17.739	15.660	12.119	15.519	14.739	16.189
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2.	12.249	11.896	15.994	16.670	16.025	13.236	13.786	14.670	15.469	15.076	16.179	14.177	15.531	17.369	12.665
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	12.612	13.558	15.512	13.904	16.139	16.125	16.991	12.710	15.670	15.691	12.365	13.546	14.325	16.994	11.923
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	11.727	16.053	17.348	13.961	17.710	15.795	14.936	12.678	13.311	10.408	16.043	18.739	16.172	10.982	10.602
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
5.	14.839	8.693	15.195	11.629	14.148	15.896	23.396	20.297	13.654	16.958	16.856	16.883	10.998	17.832	13.992
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	19.535	15.609	12.524	10.622	16.642	12.991	15.938	18.263	14.275	15.337	15.926	15.912	19.708	12.103	17.097
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	21.035	17.076	15.016	16.612	16.379	18.548	13.965	20.568	17.213	16.293	16.550	16.810	20.634	16.873	16.605
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	13.359	16.750	13.678	16.792	19.726	12.923	16.522	20.174	13.217	19.618	15.659	12.619	13.994	18.093	17.983
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	13.762	14.299	13.537	11.369	10.298	18.493	9.658	12.224	18.231	11.629	15.546	13.010	12.516	13.832	17.127
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	13.674	11.962	12.998	16.697	13.587	12.023	13.828	12.944	9.3	9.850	13.767	12.582	12.653	13.845	12.916
	136	137	138	139	200	201	202	203	204	205	206	207	208	209	210
11.	9.544	10.604	11.515	9.025	12.362	9.617	9.025	12.518	11.758	9.272	11.042	9.131	9.193	8.651	13.269
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	10.185	13.710	11.949	9.199	12.268	13.673	10.706	11.114	13.512	11.258	12.664	12.941	11.903	13.112	12.730
	126	127	128	129	140	141	142	143	144	145	146	147	148	149	150
13.	13.092	11.187	17.638	10.670	14.666	16.922	9.311	16.787	11.176	9.440	11.715	13.343	11.729	10.253	11.264
	76	77	78	79	83	81	82	83	84	85	86	87	88	89	90
14.	9.048	11.520	16.711	9.522	10.323	9.168	10.168	11.765	12.827	11.934	12.572	11.793	11.195	13.214	15.966
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	13.032	6.938	14.956	9.351	10.216	12.397	15.049	17.638	11.062	10.918	11.832	13.873	11.245	11.299	13.557

REPLICATION-2.

	24	25	26	27	28	29	100	101	102	103	104	105	106	107	108
1.	11.306	11.297	10.156	11.355	13.542	16.957	15.105	12.852	11.219	17.192	14.326	17.457	13.041	15.103	14.128
	7	31	32	46	47	76	77	78	121	135	151	166	181	196	211
2.	12.563	14.333	15.252	13.631	15.949	16.778	16.129	12.732	16.462	12.982	16.826	15.725	13.976	15.829	13.521
	9	25	39	54	69	85	99	114	129	144	159	174	189	204	219
3.	15.945	16.592	15.545	13.731	15.638	19.718	20.702	13.243	15.691	17.963	20.566	20.372	17.615	21.674	23.133
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	19.219	14.069	13.949	13.495	16.526	11.120	16.686	11.675	11.536	13.539	15.021	12.338	14.691	17.139	16.226
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	21.362	15.408	16.195	23.072	15.608	12.534	12.557	14.572	16.868	18.654	20.559	16.454	17.457	16.763	21.741
	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221
6.	18.914	12.653	16.269	17.255	18.494	16.194	17.614	13.181	10.605	13.763	18.583	12.709	10.053	14.359	16.740
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	9.724	11.824	13.668	12.029	17.711	18.256	12.585	14.907	9.462	15.462	18.104	12.127	13.248	14.232	13.650
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	19.927	21.396	16.271	14.755	22.785	19.883	15.635	16.739	22.937	16.878	18.249	19.662	14.691	15.934	20.223
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	16.650	13.326	16.944	15.277	17.736	15.596	16.248	14.795	16.199	15.238	15.529	23.691	16.792	12.627	15.672
	13	28	43	58	73	88	103	118	133	148	163	178	193	209	223
10.	13.907	14.800	15.698	11.949	12.976	19.635	11.325	13.269	15.883	15.923	21.348	17.950	14.397	18.031	22.695
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	17.952	10.204	19.332	15.778	11.894	16.858	15.083	14.962	13.845	16.348	17.513	14.322	17.134	19.248	16.647
	5	20	35	50	65	80	95	215	220	195	170	155	140	125	110
12.	13.275	18.256	13.698	12.960	16.980	15.052	23.096	25.419	17.675	21.379	12.881	16.524	19.064	19.327	17.176
	4	19	34	49	64	79	94	109	124	119	154	169	184	199	214
13.	19.721	13.751	18.660	16.719	14.415	13.511	19.348	8.611	9.229	13.029	18.780	12.209	13.523	14.404	15.423
	2	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	11.635	12.739	13.889	15.654	11.717	14.165	15.642	19.631	18.568	13.358	15.682	22.703	11.155	18.746	12.595
	15	30	45	63	75	90	105	125	135	150	165	180	195	210	225
15.	13.256	12.145	11.736	13.029	15.353	19.624	12.189	11.183	13.988	16.568	15.058	16.142	18.526	19.327	10.783

REPLICATION-3.

	83	98	23	87	101	115	129	143	157	171	185	199	213	2	16
1.	17.444	17.406	16.992	17.638	22.547	20.381	20.479	18.389	15.416	21.748	16.427	17.252	20.047	22.034	15.640
	153	166	178	192	206	220	9	23	37	51	65	79	93	107	121
2.	20.962	21.535	15.126	21.056	20.569	17.633	18.115	20.053	19.031	21.155	16.138	22.254	12.933	19.668	16.762
	88	104	118	132	146	160	174	188	202	216	5	19	33	47	61
3.	20.546	21.503	17.983	20.528	19.263	13.348	16.618	19.333	17.249	18.546	18.935	16.152	17.938	18.345	16.288
	195	209	223	12	26	93	56	60	62	95	113	129	139	152	166
4.	27.096	22.987	16.527	16.920	13.038	20.076	18.165	19.187	18.573	23.908	17.912	17.228	21.220	22.628	24.883
	185	215	133	147	161	175	189	203	217	6	20	34	48	62	76
5.	13.348	17.902	22.006	20.277	21.962	19.065	21.214	18.658	19.733	19.965	19.127	23.918	15.789	20.555	16.303
	189	194	208	222	11	25	39	53	67	41	85	139	121	137	151
6.	15.178	13.263	23.873	17.693	18.139	23.213	16.000	13.570	13.373	16.993	19.671	18.248	12.292	13.278	15.043
	88	76	88	102	116	132	146	158	172	186	202	216	3	17	33
7.	16.055	19.398	17.768	16.838	15.258	13.973	18.237	19.397	23.367	15.253	15.668	16.257	23.198	16.945	19.367
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	20.288	19.696	20.872	17.375	19.233	22.916	21.679	20.927	19.369	16.238	16.758	16.928	17.228	19.238	14.783
	229	14	28	42	56	70	84	98	112	126	140	154	168	182	196
9.	16.915	21.038	21.933	16.076	20.941	18.957	18.013	16.367	13.926	22.183	18.115	17.708	18.995	20.816	20.776
	113	149	163	177	191	205	219	9	22	36	50	64	78	92	106
10.	18.287	15.468	15.947	20.648	18.007	19.287	19.278	15.328	18.588	22.011	20.199	16.888	21.193	16.383	15.758
	165	179	193	207	221	38	24	38	52	66	80	94	108	122	136
11.	19.816	15.198	15.648	15.387	17.695	21.182	20.331	19.778	18.838	20.235	21.837	20.161	17.927	18.782	20.695
	120	136	148	162	176	190	206	218	8	21	35	49	63	77	91
12.	11.361	19.693	13.832	17.861	15.816	16.153	15.798	15.137	16.966	16.985	18.151	16.780	15.738	20.912	22.328
	35	66	58	72	86	100	114	128	142	156	170	184	198	212	3
13.	13.239	13.191	15.769	17.736	13.016	13.264	16.735	16.706	19.239	16.278	13.766	16.838	12.140	12.689	13.268
	75	89	103	117	131	145	159	171	187	201	215	6	98	32	46
14.	16.445	20.732	16.236	16.858	15.883	15.603	16.241	16.491	13.167	16.622	18.998	17.002	15.128	18.836	17.728
	216	226	93	27	41	55	69	83	97	111	125	139	153	167	181
15.	9.648	15.869	7.867	15.678	22.589	15.726	16.553	19.995	18.726	15.683	16.556	16.268	15.532	18.798	20.556

APPENDIX XIII Onset-of-heading at Parkland

PARKLAND - REPLICATION 1.

Block																	
1.	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195		
	66.000	60.000	59.000	62.000	65.000	60.000	60.000	60.000	62.000	65.000	60.000	60.000	62.000	61.000	65.000		
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30		
	60.000	60.000	59.000	60.000	62.000	63.000	60.000	60.000	60.000	58.000	57.000	61.000	60.000	60.000	62.000		
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225		
	70.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	62.000	60.000	65.000	60.000	60.000	62.000		
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60		
	62.000	60.000	60.000	62.000	60.000	60.000	60.000	61.000	62.000	60.000	60.000	60.000	60.000	60.000	60.000		
5.	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240		
	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000		
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135		
	62.000	62.000	63.000	61.000	60.000	62.000	63.000	60.000	60.000	62.000	63.000	60.000	60.000	60.000	60.000		
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105		
	63.000	63.000	60.000	61.000	60.000	61.000	63.000	60.000	60.000	60.000	60.000	60.000	62.000	60.000	60.000		
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75		
	62.000	67.000	62.000	60.000	62.000	65.000	65.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	62.000		
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165		
	60.000	62.000	60.000	62.000	65.000	62.000	60.000	60.000	60.000	60.000	60.000	65.000	62.000	60.000	60.000		
10.	2	3	4	5	6	7	8	9	10	11	12	13	14	15			
	60.000	60.000	60.000	62.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000			
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210		
	60.000	60.000	60.000	62.000	61.000	61.000	62.000	60.000	60.000	60.000	63.000	60.000	62.000	62.000	60.000		
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		
	60.000	60.000	60.000	65.000	60.000	64.000	61.000	62.000	62.000	60.000	60.000	60.000	60.000	61.000	60.000		
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150		
	60.000	60.000	63.000	62.000	62.000	65.000	60.000	64.000	64.000	60.000	60.000	62.000	62.000	62.000	60.000		
14.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90		
	67.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	60.000	62.000	60.000	60.000	60.000		
15.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180		
	66.000	60.000	60.000	65.000	66.000	66.000	63.000	63.000	60.000	60.000	60.000	62.000	60.000	62.000	60.000		

REPLICATION-2

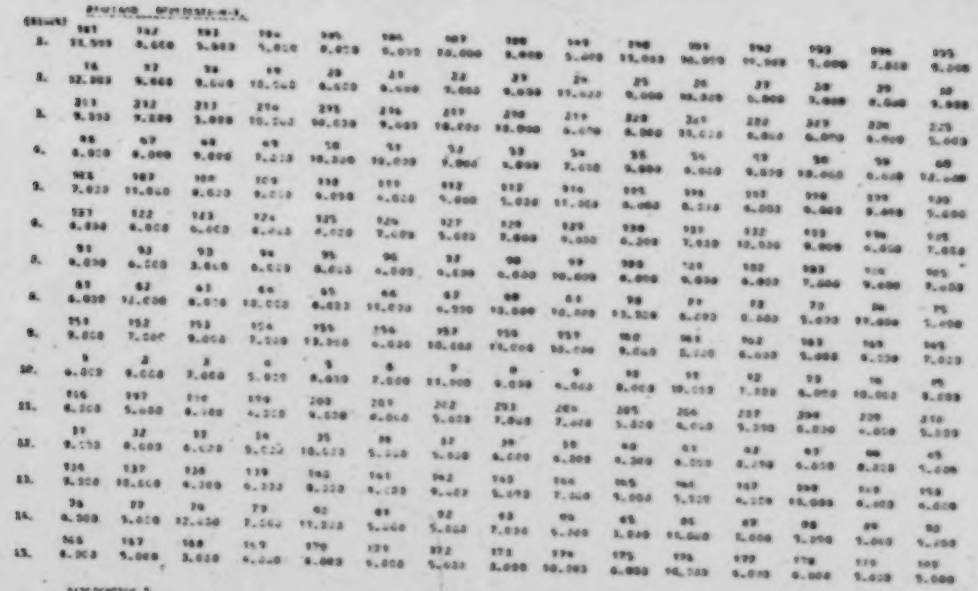
1.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90		
	68.000	66.000	69.000	69.000	68.000	66.000	66.000	67.000	67.000	66.000	67.000	69.000	68.000	66.000	67.000		
2.	1	76	77	78	79	80	81	82	83	84	85	86	87	88	89		
	69.000	69.000	69.000	67.000	67.000	67.000	69.000	69.000	68.000	67.000	67.000	69.000	68.000	68.000	67.000		
3.	1	76	77	78	79	80	81	82	83	84	85	86	87	88	89		
	68.000	67.000	67.000	69.000	66.000	67.000	69.000	68.000	69.000	68.000	66.000	66.000	67.000	68.000	68.000		
4.	2	77	12	17	62	77	92	107	122	137	152	167	182	197	212		
	66.000	66.000	66.000	66.000	63.000	67.000	69.000	74.000	68.000	69.000	69.000	69.000	68.000	68.000	68.000		
5.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216		
	66.000	68.000	69.000	67.000	67.000	69.000	67.000	68.000	68.000	67.000	66.000	68.000	67.000	67.000	67.000		
6.	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91		
	67.000	67.000	66.000	67.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
7.	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220		
	68.000	67.000	68.000	67.000	68.000	68.000	65.000	70.000	68.000	68.000	68.000	68.000	68.000	67.000	67.000		
8.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218		
	66.000	66.000	67.000	66.000	66.000	66.000	66.000	67.000	67.000	66.000	66.000	68.000	66.000	66.000	66.000		
9.	3	78	33	48	63	78	93	108	123	138	153	168	183	198	213		
	66.000	69.000	66.000	67.000	69.000	66.000	69.000	66.000	66.000	66.000	67.000	68.000	68.000	68.000	66.000		
10.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223		
	69.000	66.000	67.000	66.000	69.000	69.000	68.000	68.000	68.000	66.000	68.000	68.000	67.000	66.000	68.000		
11.	72	87	82	97	72	87	102	117	132	147	162	177	192	207	222		
	67.000	67.000	66.000	67.000	66.000	67.000	66.000	66.000	66.000	66.000	67.000	67.000	66.000	66.000	66.000		
12.	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215		
	67.000	66.000	66.000	66.000	67.000	68.000	67.000	67.000	67.000	67.000	66.000	66.000	66.000	67.000	66.000		
13.	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216		
	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
14.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221		
	67.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
15.	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218		
	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		

REPLICATION-3.

1.	45	60	75	87	102	117	132	147	162	177	192	207	222	237	252		
	66.000	66.000	67.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
2.	150	165	180	192	226	220	9	23	37	51	65	79	93	107	121		
	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
3.	58	160	210	232	196	168	176	184	202	216	5	19	33	47	61		
	66.000	66.000	66.000	66.000	66.000	67.000	66.000	67.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
4.	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166		
	66.000	67.000	66.000	67.000	66.000	66.000	66.000	66.000	66.000	67.000	66.000	66.000	67.000	66.000	66.000		
5.	181	119	131	167	183	195	180	203	219	6	20	34	48	62	76		
	66.000	62.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
6.	188	116	248	232	18	25	39	53	67	81	95	109	123	137	151		
	66.000	66.000	66.000	67.000	66.000	67.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
7.	60	76	90	102	116	130	146	160	182	196	222	236	1	17	31		
	66.000	62.000	66.000	63.000	62.000	64.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
8.	35	49	63	57	71	85	99	113	127	141	155	169	183	197	211		
	67.000	66.000	66.000	66.000	66.000	66.000	66.000	62.000	66.000	66.000	66.000	66.000	67.000	66.000	66.000		
9.	225	15	29	42	56	70	84	98	112	126	140	154	168	182	196		
	62.000	66.000	66.000	66.000	66.000	66.000	67.000	67.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
10.	135	149	163	177	193	205	219	8	22	36	50	64	78	92	106		
	66.000	66.000	66.000	62.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
11.	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136		
	62.000	66.000	66.000	63.000	67.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
12.	120	134	148	162	176	190	204	218	2	21	35	49	63	77	91		
	66.000	66.000	67.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
13.	34	48	30	72	46	100	114	128	142	156	170	184	198	212	1		
	66.000	62.000	66.000	66.000	66.000	66.000	62.000	66.000	62.000	66.000	66.000	66.000	66.000	66.000	66.000		
14.	25	39	163	177	131	145	159	173	187	201	215	6	16	32	46		
	62.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		
15.	210	224	32	27	61	95	69	83	97	111	125	139	153	167	181		
	62.000	66.000	66.000	63.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000	66.000		

APPENDIX XIV Final heading at Parkland

APPENDIX XV Heading-span at Parkland



APPENDIX XVI Plant height at Parkland

APPENDIX XVII Number of tillers per plant at Parkland

PARKLAND REPLICATION-1. NUMBER OF TILLERS PER PLANT

(Block)																
1.	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	
	15.420	12.000	13.200	12.400	16.000	11.640	12.200	12.600	11.320	11.700	11.520	12.780	12.350	15.200	13.000	
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
	12.900	12.000	14.400	14.700	13.500	15.000	12.500	12.800	11.000	13.700	13.220	14.000	14.700	13.200	12.400	
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	
	12.500	14.600	14.320	12.400	13.600	13.000	12.000	13.700	13.600	15.000	12.620	8.900	14.300	13.200	13.000	
4.	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
	14.600	11.500	12.000	13.400	10.600	14.620	12.600	15.700	12.200	12.400	12.120	12.200	12.900	15.700	14.300	
5.	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	
	15.667	13.100	13.600	12.900	11.200	15.420	10.500	13.500	14.620	11.300	12.800	15.200	12.900	11.300	13.200	
6.	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	
	15.400	12.400	12.600	14.900	10.400	12.400	13.700	11.000	11.200	12.100	14.200	14.900	12.000	10.600	12.700	
7.	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	
	10.200	13.100	14.100	12.200	9.400	10.520	14.600	13.100	14.200	13.000	12.320	12.900	10.000	13.900	12.400	
8.	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	
	15.900	14.200	13.300	10.700	11.600	14.620	13.700	13.900	14.300	12.400	14.020	10.900	11.440	14.700	13.000	
9.	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	
	11.700	15.100	12.900	12.700	13.200	13.600	14.600	12.100	11.500	13.420	11.920	13.600	12.700	10.100	12.900	
10.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
	15.900	17.100	10.400	13.600	11.900	11.720	11.320	10.300	13.600	13.100	11.600	11.600	14.100	12.900	13.600	
11.	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	
	17.100	14.000	13.100	11.100	11.500	12.420	15.600	12.900	13.500	13.400	11.220	12.500	14.400	14.200	14.700	
12.	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
	18.500	12.100	15.700	14.200	15.300	14.420	11.600	11.300	11.320	12.600	14.400	11.120	15.300	13.600	17.900	
13.	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	
	16.300	15.700	13.100	10.600	12.400	14.220	11.320	13.900	12.600	13.820	12.420	12.500	12.100	15.600	13.900	
14.	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	
	18.900	11.000	14.600	12.400	13.200	12.620	13.500	13.900	11.900	15.600	14.020	11.400	12.000	15.100	15.000	
15.	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	
	14.700	13.300	13.400	15.600	14.600	15.820	11.400	12.500	13.600	14.200	13.600	13.700	14.420	10.650	15.020	

REPLICATION-2.

1.	16	29	44	59	74	89	104	119	134	149	164	179	194	209	224	
	13.700	9.000	10.100	15.100	10.600	11.720	13.600	11.200	15.900	9.020	11.600	8.220	12.600	9.200	11.300	
2.	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211	
	15.200	11.100	12.600	10.200	12.020	11.620	11.220	13.500	9.020	12.900	10.720	12.220	9.620	10.300	13.620	
3.	9	24	39	54	69	84	99	114	129	144	159	174	189	204	219	
	14.600	15.100	13.600	14.600	11.600	10.620	12.600	11.500	12.000	11.700	10.720	15.220	12.120	12.500	11.100	
4.	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212	
	15.700	10.900	11.600	10.620	14.600	12.220	13.620	17.600	11.700	12.647	12.720	12.220	9.200	13.900	13.200	
5.	4	21	36	51	66	81	96	111	126	141	156	171	186	201	216	
	11.500	12.900	10.600	10.900	10.700	12.920	9.500	10.200	12.300	12.120	14.020	12.200	9.700	12.600	13.550	
6.	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221	
	9.600	13.220	14.500	12.600	11.600	13.920	11.700	15.900	11.300	11.600	14.220	11.200	11.600	13.500	11.950	
7.	78	25	60	55	70	85	100	115	130	145	160	175	190	205	220	
	11.620	11.600	9.700	12.600	10.500	11.600	11.900	9.500	14.300	13.600	8.500	11.600	11.700	9.600	10.720	
8.	6	23	38	53	68	83	98	113	128	143	158	173	188	203	218	
	11.600	14.200	9.100	9.900	11.200	8.600	11.700	9.500	9.600	14.500	12.500	11.700	11.600	15.600	12.600	
9.	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213	
	9.100	11.320	10.320	12.600	10.900	10.700	10.600	11.600	13.300	9.600	9.900	11.020	9.500	11.200	15.600	
10.	13	28	43	58	73	88	103	118	133	148	163	178	193	208	223	
	12.647	13.444	17.120	10.323	13.500	11.600	12.700	9.600	10.900	13.600	9.600	17.042	7.820	11.300	12.900	
11.	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222	
	12.600	13.400	8.900	7.700	9.020	9.600	12.700	10.600	10.200	8.900	15.200	6.600	11.900	9.600	10.600	
12.	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215	
	9.900	12.600	11.100	11.600	8.900	12.700	9.600	11.600	9.100	12.200	11.520	8.500	12.900	13.400	12.700	
13.	8	22	36	49	64	79	94	109	124	139	154	169	184	199	214	
	16.600	14.700	13.900	14.100	12.200	10.020	10.700	10.820	14.400	11.820	14.020	14.900	12.500	13.600	14.200	
14.	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217	
	19.200	12.900	11.100	9.620	12.020	11.600	11.600	12.400	15.200	10.300	12.620	11.900	11.900	11.600	13.700	
15.	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225	
	15.825	11.172	11.700	14.620	11.200	10.620	12.900	11.600	14.200	9.500	10.900	11.600	8.700	12.700	11.200	

REPLICATION-3.

1.	45	60	73	87	101	115	129	143	157	171	185	199	213	2	16	
	15.300	14.900	15.900	12.100	15.200	11.500	14.600	11.900	12.600	9.700	11.171	12.200	13.400	14.900	14.900	
2.	152	166	178	192	206	220	9	23	37	51	65	79	93	107	121	
	11.020	13.400	15.600	12.400	11.700	13.400	10.620	10.600	10.900	13.300	14.600	10.600	12.200	12.700	13.300	
3.	93	104	118	132	146	160	174	188	202	216	5	19	33	47	61	
	13.200	11.100	8.960	14.600	12.600	9.600	12.600	13.300	10.500	11.900	9.600	15.900	12.600	11.900	11.900	
4.	195	209	223	12	26	40	54	68	82	96	110	124	138	152	166	
	11.100	11.200	14.600	12.000	11.600	15.300	12.000	11.600	12.300	9.500	14.500	14.200	13.000	12.900	13.200	
5.	125	139	153	167	181	195	209	223	237	6	20	34	48	62	76	
	15.300	13.600	9.800	14.900	13.200	7.900	13.250	12.700	14.900	9.300	15.102	13.647	10.800	12.500	13.030	
6.	183	194	208	222	11	25	39	53	67	81	95	109	123	137	151	
	14.900	13.700	12.200	9.700	6.300	13.020	11.600	13.300	11.000	10.900	9.600	9.900	14.500	13.600	10.600	
7.	60	74	88	102	116	130	144	158	172	186	200	214	3	17	31	
	20.600	12.600	11.900	14.000	13.900	10.620	10.600	12.620	11.700	13.600	11.620	11.600	9.200	11.200	8.770	
8.	35	49	63	77	91	105	119	133	147	161	175	189	203	217	231	
	15.700	14.600	12.600	9.900	14.500	12.300	10.600	9.200	12.700	10.620	10.600	11.700	11.600	12.900	11.000	
9.	225	10	28	42	56	70	84	98	112	126	140	154	168	182	196	
	9.600	13.600	11.100	11.300	6.900	10.620	11.600	10.082	8.600	9.600	11.520	8.900	12.900	9.200	11.300	
10.	135	149	163	177	191	205	219	6	22	36	50	64	78	92	106	
	15.700	10.600	12.200	14.600	11.120	10.620	10.620	10.600	11.900	10.700	8.900	13.852	11.600	11.600	12.200	
11.	165	179	193	207	221	10	24	38	52	66	80	94	108	122	136	
	9.700	13.600	13.100	8.600	11.200	10.600	13.300	12.500	11.700	13.100	12.100	12.100	10.900	10.100	10.300	
12.	120	134	148	162	176	190	204	218	7	21	35	49	63	77	91	
	11.600	9.100	13.020	13.200	9.900	10.970	11.920	12.600	11.300	12.900	10.300	11.300	12.200	10.600	11.300	
13.	30	44	58	72	86	100	114	128	142	156	170	184	198	212	1	
	11.320	12.900	13.620	10.600	14.920	10.163	13.600	9.900	11.563	12.300	9.700	10.100	11.100	9.300	12.100	
14.	75	89	103	117	131	145	159	173	187	201	215	9	23	37	46	
	9.575	11.600	12.900	9.800	10.200	11.612	11.600	10.300	9.869	10.860	10.500	11.200	12.100	13.600	11.300	
15.	210	224	13	27	41	55	69	83	97	111	125	139	153	167	181	
	13.300	11.100	10.300	11.900	11.200	12.642	11.200	10.605	12.600	10.100	8.200	10.200	10.800	11.200	

APPENDIX XVIII Number of spikelets per spike at Parkland

APPENDIX XIX Number of seeds per spike at Parkland

Portland Application-1. Number of seeds per spike

(Block)																
1.	20.967	64.600	60.667	63.200	61.933	62.533	66.767	59.600	61.000	64.733	63.267	67.200	67.000	60.267	59.933	
2.	35 63.633	37 67.000	38 60.633	39 66.867	40 63.767	41 59.867	42 66.333	43 59.267	44 57.500	45 60.667	46 59.133	47 63.000	48 66.633	49 66.333	50 66.967	
3.	291 67.533	292 61.067	293 65.100	294 58.967	295 60.433	296 65.967	297 56.233	298 62.033	299 65.533	300 63.700	301 66.767	302 62.300	303 63.633	304 66.533	305 64.567	
4.	66 66.933	67 63.267	68 67.267	69 60.433	70 65.567	71 59.333	72 65.333	73 65.733	74 60.133	75 63.900	76 65.667	77 63.767	78 65.000	79 66.733	80 64.500	
5.	906 69.000	907 67.933	908 68.533	909 66.733	910 66.633	911 68.367	912 66.900	913 67.233	914 66.267	915 67.867	916 65.967	917 65.767	918 61.566	919 68.167	920 56.967	
6.	921 59.833	922 65.533	923 67.733	924 67.467	925 69.867	926 64.433	927 60.733	928 56.900	929 58.033	930 65.667	931 60.633	932 60.200	933 66.133	934 69.466	935 64.900	
7.	91 65.933	92 69.933	93 67.900	94 69.633	95 65.933	96 68.967	97 65.833	98 66.233	99 66.660	100 63.833	101 66.667	102 67.700	103 64.267	104 69.967	105 62.267	
8.	61 69.433	62 68.667	63 58.933	64 59.767	65 69.433	66 67.800	67 66.867	68 66.700	69 66.367	70 68.600	71 69.633	72 67.633	73 64.200	74 65.567	75 59.867	
9.	951 67.900	952 66.367	953 67.833	954 54.767	955 62.600	956 66.767	957 66.867	958 63.867	959 68.033	960 66.700	961 68.567	962 62.250	963 63.900	964 67.600	965 59.433	
10.	3 63.667	2 66.900	3 55.367	4 68.733	5 58.233	6 69.670	7 55.033	8 67.933	9 68.033	10 32.133	11 67.233	12 66.067	13 68.067	14 66.000	15 66.000	
11.	196 58.067	197 68.067	198 56.633	199 66.567	200 67.667	201 67.933	202 66.167	203 30.633	204 58.767	205 63.233	206 58.967	207 63.833	208 62.633	209 65.367	210 67.300	
12.	31 64.533	32 66.500	33 65.767	34 62.233	35 59.930	36 66.667	37 67.333	38 65.233	39 62.700	40 66.500	41 66.767	42 65.567	43 63.267	44 65.533	45 56.667	
13.	126 64.467	127 65.533	128 68.200	129 56.633	130 67.967	131 65.533	132 58.967	133 58.767	134 69.033	135 36.267	136 66.533	137 66.233	138 66.500	139 65.067	140 56.033	
14.	76 65.767	77 67.733	78 58.533	79 65.033	80 63.533	81 66.633	82 66.467	83 69.067	84 66.567	85 61.033	86 65.600	87 65.633	88 58.230	89 65.767	90 68.250	
15.	146 59.633	147 59.333	148 62.967	149 60.533	150 58.500	151 66.300	152 61.900	153 64.967	154 67.333	155 65.633	156 67.333	157 61.000	158 59.967	159 67.300	160 59.367	

Application-2.

1.	98 66.833	99 60.600	100 61.333	101 62.600	102 65.633	103 60.967	104 59.133	105 62.967	106 63.267	107 66.233	108 66.000	109 66.700	110 62.033	111 65.367	112 63.733	
2.	1 65.767	78 66.767	77 67.600	76 61.967	75 61.600	74 58.867	73 59.267	72 66.600	71 65.633	70 66.767	69 66.633	68 56.267	67 66.767	66 66.100	65 61.767	
3.	9 66.833	20 61.700	29 62.767	54 61.933	69 58.967	86 66.900	99 61.200	114 66.933	129 67.133	144 59.567	159 58.933	174 62.700	189 61.033	204 65.600	219 61.233	
4.	2 58.933	17 65.867	32 66.200	47 62.933	62 57.633	77 59.767	92 66.533	107 66.267	122 66.767	137 68.533	152 66.767	167 61.367	182 59.650	197 56.233	212 56.600	
5.	6 52.700	21 55.767	36 66.533	51 67.833	66 66.767	81 65.500	96 65.767	111 51.733	126 65.633	141 61.267	156 66.550	171 66.767	186 61.300	201 65.867	216 67.967	
6.	10 67.933	25 66.800	40 65.700	55 52.633	70 66.767	85 68.633	100 65.633	115 65.367	130 66.533	145 58.633	160 66.267	175 58.733	190 68.233	205 66.767	220 66.900	
7.	14 62.833	29 52.650	44 58.967	59 66.133	74 65.567	89 60.633	104 61.600	119 67.233	134 63.133	149 65.767	164 66.267	179 66.967	194 65.267	209 65.133	224 56.833	
8.	15 59.733	30 63.933	45 66.633	60 66.233	75 62.933	90 61.900	105 63.133	120 62.367	135 63.933	150 66.633	165 59.933	180 65.933	195 61.967	210 67.167	225 61.967	
9.	3 65.533	18 66.200	33 65.650	48 63.767	63 58.267	78 65.533	93 63.767	108 58.067	123 62.767	138 65.600	153 66.900	168 62.633	183 66.767	198 61.867	213 58.650	
10.	22 62.533	37 58.866	52 62.250	67 62.666	82 65.639	97 66.250	112 66.333	127 66.833	142 66.133	157 52.667	172 66.833	187 62.300	202 62.667	217 66.567	232 65.767	
11.	92 58.250	27 65.233	42 35.967	57 66.633	72 65.967	87 67.267	102 66.633	117 65.867	132 65.400	147 67.167	162 65.767	177 39.567	192 39.533	207 39.167	222 67.600	
12.	5 67.350	20 66.750	35 35.733	50 65.950	65 66.950	80 66.967	95 66.255	110 66.833	125 59.533	140 62.967	155 66.967	170 65.250	185 66.733	200 66.833	215 66.150	
13.	6 67.667	79 67.833	36 67.967	63 62.767	66 66.267	79 66.991	96 29.700	109 66.765	126 66.667	139 66.650	156 66.950	169 67.233	186 66.183	199 66.833	216 66.667	
14.	7 66.867	22 66.260	37 58.450	52 65.267	67 52.850	82 65.667	97 66.933	112 58.267	127 56.867	142 62.433	157 62.767	172 66.183	187 66.650	202 52.433	217 56.533	
15.	15 62.950	30 62.833	45 58.767	60 66.633	75 67.300	90 66.533	105 62.550	120 66.933	135 66.633	150 67.650	165 66.533	180 66.367	195 66.667	210 66.867	225 62.850	

Application-3.

1.	65 66.633	80 66.767	95 66.900	97 35.733	100 35.150	115 66.967	130 66.250	145 62.500	160 58.967	175 65.567	190 61.650	205 62.850	220 66.967	5 65.867	20 58.133	
2.	155 62.833	156 66.150	170 65.867	192 30.167	206 66.833	220 66.867	0 66.167	29 36.734	37 62.867	50 66.633	65 66.267	78 61.833	93 66.150	107 67.633	120 66.833	
3.	93 66.733	106 67.333	119 69.867	132 66.967	146 66.523	160 39.650	170 62.133	160 36.667	203 58.567	218 37.950	5 61.500	19 65.333	33 39.500	47 36.200	61 35.200	
4.	195 58.833	209 66.450	223 66.267	12 55.650	26 65.633	40 66.333	54 66.733	68 62.900	82 66.233	95 57.300	110 62.333	124 65.233	138 39.767	152 61.867	166 66.167	
5.	205 66.200	219 67.700	233 35.633	247 36.467	261 65.533	275 67.333	289 66.533	303 62.650	317 66.867	6 37.367	20 62.950	34 36.333	48 39.967	62 66.333	76 65.533	
6.	203 67.333	218 66.367	233 65.633	248 36.333	263 66.333	278 66.950	293 61.967	308 67.967	323 67.850	83 65.767	93 65.700	109 66.650	123 66.633	137 66.367	151 66.533	
7.	63 66.767	76 67.967	88 65.633	102 66.267	116 66.767	130 66.633	144 66.950	158 63.650	172 62.667	185 65.233	200 54.767	214 26.550	1 67.933	17 38.333	31 65.650	
8.	35 65.767	49 65.833	63 35.967	78 65.767	93 56.867	107 66.250	121 67.650	135 66.667	149 52.400	163 62.350	177 61.550	191 52.133	205 67.500	219 66.367	233 66.000	
9.	245 67.650	259 39.267	273 65.667	287 66.767	301 66.650	315 67.933	329 66.150	343 65.350	357 67.967	370 67.950	384 65.650	398 65.833	412 67.967	426 66.100	440 67.650	
10.	335 65.950	349 38.967	363 36.533	377 67.833	391 66.867	405 70.967	419 66.500	6 66.250	22 66.533	36 66.533	50 62.933	64 58.267	78 66.533	92 65.600	106 66.700	
11.	365 62.267	378 65.333	392 67.833	407 36.333	421 35.666	50 65.533	29 62.967	38 65.950	53 66.867	66 62.867	80 37.900	94 66.633	108 35.333	122 66.833	136 62.900	
12.	320 66.833	334 63.967	348 66.867	362 66.633	376 65.833	390 66.767	404 62.867	418 36.533	7 62.867	21 65.567	35 65.100	49 66.967	63 61.350	77 35.333	91 66.667	
13.	90 66.150	90 63.367	56 66.833	73 62.500	88 63.300	103 35.233	134 66.533	149 65.667	163 65.833	176 58.950	190 67.833	204 66.567	218 35.967	232 62.867	5 62.867	
14.	75 58.450	89 65.733	103 66.867	117 59.500	131 65.333	145 35.933	159 66.233	173 62.733	187 66.350	201 63.833	215 66.233	0 58.500	30 66.500	32 65.633	46 35.167	
15.	216 66.167	229 66.867	13 65.767	27 65.833	41 61.300	55 66.133	69 66.133	83 65.667	97 66.933	111 67.833	125 52.833	139 65.300	153 35.633	167 66.233	181 61.500	

APPENDIX XX Weight of seeds per spike at Parkland

(Blocks)																
1.	181 0.547	182 0.611	183 0.569	184 0.725	185 0.669	186 0.776	187 0.585	188 0.965	189 0.654	190 0.358	191 0.696	192 0.886	193 0.389	194 0.819	195 0.837
2.	16 0.959	17 0.858	18 0.661	19 0.536	20 0.326	21 0.643	22 0.763	23 0.663	24 0.599	25 0.679	26 0.189	27 0.923	28 0.668	29 0.367	30 0.605
3.	211 0.769	212 0.563	213 0.771	214 0.455	215 0.954	216 0.668	217 0.948	218 0.693	219 0.936	220 0.731	221 0.396	222 0.647	223 0.674	224 0.647	225 0.868
4.	46 0.754	47 0.536	48 0.999	49 0.631	50 2.058	51 0.457	52 0.668	53 0.735	54 1.761	55 0.494	56 2.237	57 0.525	58 0.729	59 0.815	60 0.757
5.	106 0.952	107 0.946	108 0.692	109 0.716	110 0.455	111 0.668	112 0.626	113 0.676	114 0.835	115 0.565	116 0.750	117 0.635	118 0.960	119 0.672	120 0.598
6.	121 0.648	122 0.697	123 0.722	124 0.715	125 0.771	126 0.679	127 0.954	128 0.961	129 0.997	130 0.658	131 0.645	132 0.773	133 0.694	134 0.661	135 0.695
7.	91 0.809	92 0.573	93 0.781	94 0.588	95 0.764	96 0.650	97 0.567	98 0.624	99 0.650	100 0.598	101 0.606	102 0.565	103 0.586	104 0.558	105 0.569
8.	61 0.528	62 0.553	63 0.753	64 0.926	65 0.723	66 0.665	67 0.765	68 0.720	69 0.729	70 0.251	71 0.705	72 0.618	73 0.634	74 0.519	75 0.573
9.	151 0.871	152 0.663	153 0.696	154 0.663	155 0.516	156 0.579	157 0.573	158 0.344	159 0.852	160 0.936	161 0.733	162 0.659	163 0.595	164 0.761	165 0.908
10.	1 0.695	2 0.744	3 2.916	4 0.593	5 0.992	6 0.661	7 0.565	8 0.618	9 0.895	10 0.572	11 0.793	12 0.539	13 0.606	14 0.8.8	15 0.632
11.	196 0.699	197 0.532	198 0.966	199 0.574	200 0.602	201 0.653	202 0.725	203 0.697	204 2.021	205 0.537	206 2.125	207 0.615	208 0.523	209 0.773	210 0.574
12.	31 0.964	32 0.760	33 0.833	34 0.368	35 0.375	36 0.626	37 0.613	38 0.673	39 0.926	40 0.605	41 0.796	42 0.529	43 0.828	44 0.849	45 0.789
13.	136 0.668	137 0.665	138 0.819	139 0.909	140 0.676	141 0.723	142 0.879	143 0.845	144 2.076	145 0.827	146 0.563	147 0.672	148 0.793	149 0.529	150 0.765
14.	76 0.666	77 0.765	78 0.569	79 0.648	80 0.393	81 0.681	82 0.519	83 0.659	84 0.965	85 0.672	86 0.915	87 0.763	88 0.523	89 0.695	90 0.687
15.	166 0.719	167 0.596	168 0.402	169 0.824	170 0.136	171 0.772	172 0.665	173 0.768	174 0.327	175 0.384	176 0.629	177 0.525	178 0.651	179 0.667	180 0.628

REPLICATION-2.

1.	16 0.362	17 0.669	18 0.509	19 0.526	20 0.375	21 0.771	22 0.390	23 0.650	24 0.693	25 0.616	26 0.556	27 0.643	28 0.620	29 0.612	30 0.554
2.	1 0.755	16 0.679	31 0.550	46 0.722	61 0.602	76 0.750	91 0.822	106 0.960	121 0.546	136 0.206	151 0.759	166 0.806	181 0.292	196 0.7.8	211 0.650
3.	9 0.836	24 0.961	39 0.661	54 0.326	69 0.675	84 0.626	99 0.573	114 0.372	129 0.878	144 0.699	159 2.118	174 0.643	189 1.332	204 0.803	219 0.693
4.	2 2.991	17 0.792	32 0.825	47 0.503	62 0.629	77 0.223	92 0.810	107 0.562	122 0.597	137 0.607	152 0.529	167 0.625	182 0.569	197 0.2.0	212 0.207
5.	6 2.176	21 0.676	36 0.807	51 0.723	66 0.555	81 0.611	96 0.903	111 0.609	126 0.601	141 0.752	156 0.352	171 0.643	186 0.738	201 0.5.3	216 0.869
6.	11 0.671	26 0.988	41 2.077	56 0.969	71 0.706	86 0.700	101 0.716	116 0.552	131 0.867	146 2.054	161 0.656	176 0.706	191 0.745	206 0.6.0	221 0.506
7.	30 0.820	25 0.683	40 0.687	55 0.524	70 0.655	85 0.629	100 0.999	115 0.696	130 0.926	145 0.867	160 0.636	175 0.672	190 0.900	205 0.6.7	220 0.790
8.	8 0.510	23 0.565	38 0.639	53 0.540	68 0.756	83 0.594	98 0.660	113 0.640	128 0.656	143 0.911	158 0.720	173 0.721	188 0.664	203 0.7.2	218 0.636
9.	3 2.951	18 0.722	33 0.960	48 0.927	63 0.961	78 0.529	93 0.682	108 0.662	123 0.569	138 0.909	153 0.666	168 0.768	183 0.611	198 0.6.0	213 0.938
10.	15 0.799	30 0.569	45 0.730	60 0.592	75 0.693	90 0.653	105 0.326	120 0.618	135 0.601	150 0.658	165 0.632	180 0.617	195 0.639	210 0.6.2	225 0.642
11.	12 0.750	27 0.723	42 0.669	57 0.822	72 0.695	87 0.763	102 0.781	117 0.696	132 0.756	147 0.908	162 0.779	177 0.708	192 0.696	207 0.6.9	222 0.695
12.	5 0.668	20 0.739	35 0.237	50 0.976	65 0.857	80 0.660	95 0.817	110 0.822	125 0.975	140 0.331	155 0.569	170 0.709	185 0.659	200 0.5.9	215 0.769
13.	6 0.613	21 0.669	36 0.857	51 0.765	66 1.219	81 0.766	96 0.625	111 0.663	126 0.569	141 0.930	156 0.614	171 0.716	186 0.598	201 0.7.7	216 0.639
14.	7 0.516	22 0.713	37 2.916	52 0.673	67 0.791	82 0.657	97 0.556	112 0.796	127 0.622	142 0.769	157 0.622	172 0.219	187 0.508	202 0.7.3	217 0.673
15.	15 0.672	31 0.829	45 0.872	60 0.698	75 0.808	90 0.930	105 0.617	120 0.705	135 0.965	150 0.875	165 0.903	180 0.618	195 0.869	210 0.652	225 0.593

REPLICATION-3.

1.	45 0.668	59 0.252	73 0.346	87 0.855	101 0.252	115 1.695	129 0.565	143 0.682	157 2.022	171 0.560	185 0.829	199 1.119	213 1.669	2 1.994	16 0.899
2.	150 1.022	164 0.556	178 0.760	192 1.219	206 0.966	223 0.563	0 1.337	23 1.120	37 0.913	51 0.628	65 0.661	79 0.799	93 0.619	107 1.321	121 1.378
3.	90 0.673	104 2.069	118 0.553	132 0.663	146 0.792	163 0.573	179 0.265	194 0.725	232 2.130	246 0.693	5 0.715	19 0.691	33 0.268	47 0.677	61 0.968
4.	195 0.918	209 0.858	223 0.892	32 0.765	46 0.716	60 0.506	56 0.532	68 0.626	92 0.655	96 0.955	110 0.660	124 0.819	138 0.469	152 0.583	166 0.522
5.	105 0.550	119 0.752	133 0.603	147 1.279	161 0.505	175 1.725	189 0.766	203 0.667	217 0.678	6 0.658	20 0.655	34 0.519	48 0.146	62 0.268	76 0.960
6.	200 0.586	166 0.570	208 0.799	222 1.253	31 0.568	45 1.697	59 0.918	53 0.606	67 0.295	81 0.665	95 0.259	109 0.586	120 0.657	137 0.557	151 0.952
7.	66 0.562	76 0.875	66 0.669	102 0.660	116 0.611	132 0.251	146 0.712	160 0.683	222 0.665	185 0.668	203 0.753	216 0.562	3 2.206	17 0.721	31 0.783
8.	45 0.593	29 0.669	43 0.861	57 0.918	71 0.696	85 0.657	99 0.766	113 0.866	127 0.918	141 0.668	155 0.181	169 0.759	183 0.586	197 0.772	211 0.657
9.	225 0.646	14 0.783	28 0.655	42 0.561	56 2.328	70 0.668	84 0.652	98 0.863	112 0.839	126 0.766	140 0.652	154 0.956	168 0.668	182 0.873	196 0.698
10.	135 0.785	149 1.726	163 0.565	177 2.116	191 0.729	205 0.765	219 0.567	0 2.049	22 0.847	36 0.656	50 0.583	64 0.968	78 0.669	92 0.626	106 0.299
11.	165 0.657	179 0.711	193 2.020	207 0.150	221 0.956	10 0.537	24 0.736	38 0.000	52 0.676	66 0.653	80 0.250	94 0.550	108 0.588	122 0.912	136 0.523
12.	120 0.577	134 0.653	148 0.563	162 0.676	176 0.876	190 0.970	204 0.596	218 0.568	7 0.235	21 0.593	35 0.736	49 0.665	63 0.719	77 0.125	91 2.072
13.	30 0.710	44 0.557	58 0.761	72 0.620	86 0.668	100 0.626	114 0.581	128 0.609	142 0.665	156 0.719	170 0.672	184 0.692	198 0.836	212 0.674	3 0.693
14.	75 0.751	89 0.611	103 0.765	117 0.706	131 0.956	145 0.526	159 0.519	173 0.723	187 0.652	201 0.650	215 0.650	6 0.870	20 0.572	34 0.561	48 0.677
15.	210 0.732	224 0.527	11 0.696	25 0.660	41 0.623	55 0.636	69 0.629	83 0.676	97 0.792	111 0.727	125 0.958	139 0.750	153 0.395	167 0.690	181 0.573

APPENDIX XXI 1000-kernel weight at Parkland

PARKLAND REPLICATION-1. 1000-KERNEL WEIGHT

(Block)																
	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	
1.	39.696	38.163	38.387	36.476	37.698	41.915	36.225	38.128	39.068	38.082	38.357	40.188	37.742	35.578	35.956	
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
2.	36.363	39.589	36.432	36.363	39.768	42.705	39.953	39.748	42.638	37.592	40.093	37.038	36.326	37.638	38.583	
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	
3.	36.992	39.892	40.206	38.968	40.338	40.586	38.638	37.076	42.047	35.153	36.333	38.888	38.216	38.569	38.511	
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	
4.	37.462	35.938	42.332	36.539	41.956	36.915	36.738	38.698	35.769	38.772	40.826	37.838	37.458	37.938	36.595	
	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	
5.	39.962	35.518	38.316	36.623	38.426	36.062	35.769	35.553	36.829	36.838	39.798	35.296	36.615	38.772	39.985	
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	
6.	38.788	37.208	36.352	35.386	36.641	38.357	36.198	38.958	38.528	42.836	38.663	35.382	38.398	37.648	36.568	
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	
7.	39.838	39.386	36.676	38.712	38.658	38.512	38.418	38.218	40.858	38.677	38.611	35.869	36.820	38.959	36.385	
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	
8.	38.565	38.742	38.582	35.358	38.338	36.196	37.458	36.788	37.288	38.748	36.458	38.938	38.726	38.208	38.578	
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	
9.	40.598	38.697	38.525	38.588	37.485	38.388	38.188	37.868	37.298	38.945	38.478	38.538	38.943	38.388	38.828	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
10.	38.618	38.823	38.838	38.558	38.618	38.807	38.588	38.788	38.855	38.852	38.168	38.138	38.248	38.838	38.885	
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	
11.	37.278	38.118	36.521	36.638	38.818	38.818	36.735	38.266	38.638	38.185	38.183	36.388	36.638	38.898	38.338	
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
12.	37.766	37.668	38.838	38.518	38.458	38.838	38.722	36.918	38.828	38.883	42.665	37.887	36.248	38.262	38.712	
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	
13.	40.786	38.758	37.968	38.428	38.448	37.682	36.187	37.653	42.388	38.995	38.238	38.768	38.868	38.838	38.855	
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	
14.	38.628	38.687	38.838	37.218	38.262	38.228	38.728	37.198	38.888	38.662	38.938	38.328	38.928	38.768	38.668	
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	
15.	38.661	38.238	38.138	36.718	38.278	38.548	38.838	38.888	38.838	38.628	38.328	38.758	38.682	38.768	38.488	

REPLICATION-2.

	16	29	44	59	76	89	104	119	134	149	164	179	194	209	224	
1.	38.618	37.462	36.735	35.335	38.275	38.928	35.883	38.838	29.716	35.528	36.768	38.238	38.856	38.768	37.654	
	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211	
2.	38.268	40.891	38.387	42.883	38.615	35.352	36.372	32.188	33.282	38.823	41.413	32.668	37.218	38.332	38.782	
	9	26	39	56	69	86	93	116	126	146	155	176	189	206	219	
3.	38.251	42.856	38.193	38.888	36.366	36.153	36.378	32.658	38.836	42.855	42.875	38.738	37.846	38.218	35.853	
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212	
4.	42.768	38.835	40.768	37.328	38.758	32.963	38.492	38.838	36.875	38.812	38.362	38.886	38.558	36.576	32.868	
	6	21	36	51	66	81	96	111	126	141	156	171	186	201	216	
5.	42.237	38.168	38.458	35.825	42.838	36.358	42.838	32.568	35.165	42.478	38.568	38.887	38.888	38.832	38.868	
	11	26	41	56	71	86	101	116	131	146	161	176	191	206	221	
6.	37.823	42.528	45.452	37.815	40.628	36.736	38.228	38.878	38.885	42.781	38.926	35.368	36.728	37.268	32.912	
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220	
7.	42.312	38.248	38.636	38.788	38.668	38.828	36.718	42.728	38.878	37.185	38.828	38.612	36.818	38.898	38.842	
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218	
8.	38.768	38.278	38.396	38.238	42.178	38.188	38.858	38.858	38.618	40.388	38.838	38.858	38.628	38.898	38.826	
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213	
9.	42.278	38.198	42.868	42.877	38.788	38.852	38.388	42.568	38.288	38.838	38.958	37.398	37.598	38.488	38.178	
	12	28	43	58	73	88	103	118	133	148	163	178	193	208	223	
10.	38.492	38.868	41.268	38.648	38.528	40.298	38.728	42.868	41.958	38.128	38.678	38.868	38.948	38.738	38.188	
	31	27	42	57	72	87	102	117	132	147	162	177	192	207	222	
11.	38.328	37.968	38.468	40.128	41.238	38.798	38.968	38.878	38.598	38.838	37.928	38.858	37.958	37.638	38.948	
	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215	
12.	38.418	38.828	37.878	40.648	41.838	38.312	41.868	42.788	38.298	38.432	38.758	38.238	38.732	38.358	40.878	
	4	19	34	49	64	79	94	109	124	139	154	169	184	199	214	
13.	38.838	38.838	38.188	38.888	38.888	38.868	38.268	38.888	38.878	37.838	38.768	38.888	38.878	38.588	38.868	
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217	
14.	37.942	38.988	37.858	42.828	38.858	38.558	38.388	38.858	38.788	42.828	38.588	38.828	38.738	38.988	38.178	
	15	30	45	60	75	90	105	120	135	150	165	180	195	210	225	
15.	38.568	38.188	37.258	38.838	38.668	38.178	38.128	38.388	38.268	38.858	38.738	38.658	37.388	38.178	38.968	

REPLICATION-3.

	45	58	73	87	101	115	129	143	157	171	185	199	213	2	15	
1.	39.338	37.376	38.592	40.162	38.798	41.668	38.385	38.385	38.158	38.562	38.788	38.868	38.968	42.868	38.618	
	150	166	178	192	206	220	9	23	37	53	65	80	93	108	121	
2.	38.988	38.358	38.538	38.518	38.728	38.638	38.868	38.668	38.868	38.928	38.862	38.252	38.838	38.218	38.138	
	93	106	118	132	146	160	173	188	202	216	5	18	31	47	61	
3.	38.838	38.778	38.548	38.878	40.518	38.388	38.688	38.248	42.868	38.248	38.768	38.838	38.868	38.288	38.578	
	195	208	223	12	26	38	50	68	82	96	110	126	138	152	166	
4.	38.698	40.378	40.678	38.688	37.878	38.758	38.388	38.788	38.388	38.588	38.282	40.828	38.578	38.888	38.788	
	195	210	222	242	258	275	289	231	252	6	28	36	48	62	76	
5.	38.688	38.588	37.818	37.588	38.678	38.282	40.858	42.568	38.358	38.678	38.268	38.838	38.278	38.858	38.198	
	185	198	208	222	11	25	39	53	67	81	95	120	123	138	153	
6.	38.788	38.228	38.188	38.382	38.268	38.668	37.588	38.788	38.458	38.528	38.818	38.788	38.668	38.878	38.282	
	83	76	88	102	116	130	144	158	172	186	200	214	3	17	31	
7.	38.258	38.878	38.188	38.788	38.778	38.278	38.588	38.278	38.838	37.852	38.818	38.828	38.738	38.888	38.782	
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211	
8.	38.888	38.828	38.668	42.818	38.238	38.728	38.858	38.788	38.388	38.788	38.128	38.868	38.872	38.868	38.388	
	125	19	28	42	56	70	84	98	112	126	140	154	168	182	196	
9.	38.868	38.928	38.838	38.788	42.858	38.888	38.888	38.888	38.888	38.388	38.588	38.858	38.858	38.738	38.388	
	135	149	163	179	191	205	219	8	22	36	50	64	78	92	106	
10.	38.988	38.868	38.338	42.788	38.858	38.778	38.878	41.868	38.898	38.288	38.878	38.388	38.528	38.878	38.688	
	153	170	183	207	220	38	24	38	52	66	80	94	108	122	136	
11.	38.588	37.788	42.828	37.138	41.318	38.548	38.878	38.778	42.128	38.288	38.872	38.858	38.878	38.388	38.858	
	123	138	148	162	176	190	204	218	3	21	35	49	63	77	91	
12.	38.898	38.288	38.828	38.858	38.858	42.898	37.218	42.568	38.388	38.788	38.788	38.868	38.818	38.832	42.578	
	35	48	58	72	86	100	114	128	142	156	170	184	198	212	1	
13.	38.728	38.118	38.738	37.928	38.188	38.868	38.488	38.868	38.338	38.892	38.858	38.288	38.858	38.188	38.288	
	25	39	103	117	131	145	159	173	187	201	215	6	36	32	46	
14.	38.212	38.868	38.852	38.268	38.528	37.748	37.928	42.888	38.488	37.818	42.858	38.288	38.578	37.868	38.828	
	218	228	13	27	41	55	69	83	97	111	125	139	153	167	180	
15.	38.488	38.788	37.318	38.522	38.568	42.978	38.538	37.868	38.778	38.838	38.381	38.328	38.868	38.968	37.792	

APPENDIX XXII Yield per plant at Parkland

PARKLAND AGRICULTURAL STATION - YIELD PER PLANT

(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	16.548	20.077	16.595	17.922	20.963	19.037	17.917	16.660	16.646	15.351	15.292	12.253	15.039	15.410	20.652
	96	97	98	99	20	21	22	23	24	25	26	27	28	29	30
2.	16.563	17.710	14.230	11.550	12.880	16.533	19.536	13.091	16.866	11.997	17.108	20.131	17.329	23.231	13.649
	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
3.	16.619	13.196	16.327	12.167	16.705	15.975	13.061	11.536	15.319	14.862	12.569	12.355	15.006	13.726	16.769
	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
4.	17.705	16.692	16.639	22.533	25.113	16.168	19.674	16.625	16.669	13.672	15.876	18.980	13.056	11.062	17.959
	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
5.	19.321	16.326	14.822	15.165	15.676	20.025	19.028	11.951	23.244	17.811	22.999	13.715	13.687	13.749	16.818
	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135
6.	17.626	19.567	17.976	11.749	14.662	12.601	15.563	16.677	17.742	19.257	24.775	16.783	14.219	13.716	20.252
	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105
7.	17.935	16.324	15.853	12.695	11.760	14.242	19.092	16.193	19.189	13.915	11.670	11.621	16.513	16.694	15.228
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
8.	16.622	13.1.6	14.008	11.263	12.692	13.664	15.214	16.357	14.329	11.754	15.075	12.153	15.248	13.729	14.379
	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165
9.	16.847	19.611	15.536	13.658	13.636	12.660	15.095	11.936	13.726	13.711	12.659	13.369	13.290	12.728	15.185
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
10.	17.983	20.692	15.671	17.135	16.116	15.239	13.093	12.760	11.758	9.118	14.323	11.226	14.743	13.420	13.829
	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
11.	15.111	13.532	14.643	11.715	12.133	15.656	15.271	15.615	18.210	15.333	14.493	12.732	14.159	15.619	17.946
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
12.	14.941	15.139	15.422	13.361	20.228	15.105	12.539	11.827	12.413	10.619	15.546	12.645	13.348	14.596	11.428
	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
13.	18.536	15.149	17.751	12.965	14.814	19.289	15.744	16.795	19.237	12.345	12.611	12.652	11.714	15.382	16.156
	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
14.	16.698	13.516	12.619	11.658	11.723	11.529	13.706	14.785	8.256	14.855	12.563	12.602	13.616	13.668	17.652
	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
15.	16.176	16.162	15.567	15.009	16.167	15.555	16.269	13.357	12.810	12.749	14.257	15.609	15.195	14.833	13.324

APPLICATION-2.

	16	29	44	59	76	89	104	119	134	149	164	179	194	209	224
1.	9.959	12.058	14.127	1..	8.527	17.511	10.763	14.078	11.825	10.227	11.443	12.260	13.721	13.124	11.198
	1	16	31	46	61	76	91	106	121	136	151	166	181	196	211
2.	12.122	14.233	12.219	12.573	11.495	14.600	14.641	11.642	11.241	10.076	14.540	11.858	8.033	13.665	11.453
	3	20	35	50	65	80	95	110	125	140	155	170	185	200	215
3.	13.597	14.262	14.358	11.981	13.156	14.655	13.504	14.242	14.329	10.156	15.670	13.267	12.153	13.612	12.572
	2	17	32	47	62	77	92	107	122	137	152	167	182	197	212
4.	14.431	13.599	14.905	12.226	14.632	11.995	14.672	14.013	12.502	13.144	13.279	15.721	9.623	13.825	11.126
	5	21	36	51	66	81	96	111	126	141	156	171	186	201	216
5.	15.511	14.196	12.240	14.648	12.868	15.525	14.515	14.128	12.652	11.823	13.776	11.316	14.426	13.612	11.829
	33	35	50	54	71	96	101	116	131	146	161	176	191	206	221
6.	15.526	14.519	23.197	15.668	14.246	13.776	13.316	17.027	14.618	12.239	13.693	15.056	15.663	14.349	17.767
	10	25	40	55	70	85	100	115	130	145	160	175	190	205	220
7.	11.675	13.328	11.255	12.217	10.660	12.633	15.691	14.249	12.774	14.671	11.670	13.202	11.665	11.742	12.729
	8	23	38	53	68	83	98	113	128	143	158	173	188	203	218
8.	13.067	20.687	13.215	15.281	15.570	16.019	16.277	12.552	15.796	16.449	14.661	13.506	15.239	14.021	12.245
	3	18	33	48	63	78	93	108	123	138	153	168	183	198	213
9.	16.389	14.665	13.766	20.655	19.703	13.533	14.722	14.276	13.279	15.263	12.193	13.658	11.219	13.144	13.772
	22	39	42	58	73	88	103	118	133	148	163	178	193	208	223
10.	21.773	25.479	20.698	12.667	15.319	15.632	16.681	17.443	17.197	16.616	12.179	15.756	13.327	11.661	14.152
	12	27	42	57	72	87	102	117	132	147	162	177	192	207	222
11.	12.923	14.696	10.172	11.565	12.265	17.433	14.434	14.857	14.219	13.552	14.595	14.276	8.679	9.918	15.292
	5	20	35	50	65	80	95	110	125	140	155	170	185	200	215
12.	12.294	17.228	10.914	15.166	11.519	14.339	14.260	13.366	13.457	11.913	13.705	13....	12.170	13.681	23.615
	6	23	36	49	64	79	94	109	124	139	154	169	184	199	214
13.	15.768	13.121	15.235	12.253	14.376	12.716	14.620	11.583	13.279	13.230	15.216	14.177	12.227	11.662	11.972
	7	22	37	52	67	82	97	112	127	142	157	172	187	202	217
14.	16.367	19.269	10.369	13.223	11.448	12.272	10.220	14.614	10.363	13.699	12.653	14.078	13.763	13.328	12.676
	55	70	85	100	115	130	145	160	175	190	205	220	235	250	265
15.	12.025	13.277	13.926	17.049	14.028	14.450	14.266	15.765	20.035	15.552	14.928	14.037	11.209	11.483	12.918

APPLICATION-3.

	45	59	33	47	101	115	129	143	157	171	185	199	213	2	16
1.	10.815	9.946	14.643	9.640	11.121	14.193	12.650	11.103	17.276	11.020	14.202	14.220	14.126	14.162	13.993
	150	166	178	192	206	220	9	23	37	51	65	79	93	107	121
2.	10.611	14.519	17.091	8.960	11.562	13.691	13.265	10.608	14.767	15.130	11.581	8.193	13.452	13.882	13.009
	90	104	118	132	146	163	176	190	202	216	5	19	33	47	61
3.	12.966	14.031	12.193	23.020	15.643	12.5..	10.738	11.295	14.666	9.652	11.583	17.023	15.026	15.198	9.963
	195	209	221	93	26	40	54	68	82	96	112	126	139	092	166
4.	14.263	18.611	15.161	15.057	11.521	14.210	11.068	13.203	11.674	14.110	12.762	12.127	13.748	14.493	13.152
	109	119	133	147	161	175	189	203	217	6	20	34	48	62	76
5.	13.783	13.652	12.652	14.322	11.325	12.091	14.652	12.492	14.363	10.535	11.995	9.360	11.267	9.178	9.219
	166	194	208	222	11	25	39	53	67	81	95	109	123	137	151
6.	11.448	13.762	14.915	11.337	13.720	13.261	20.095	12.073	8.953	9.932	8.258	12.033	17.261	15.710	13.363
	60	76	90	102	116	130	144	158	172	186	200	214	3	17	31
7.	13.526	11.294	15.222	11.258	14.020	8.717	14.667	11.078	15.241	12.225	17.211	15.326	13.035	13.599	12.620
	15	29	43	57	71	85	99	113	127	141	155	169	183	197	211
8.	12.953	13.140	13.614	13.778	17.423	14.234	14.515	12.006	15.216	12.758	11.745	14.153	12.315	13.033	14.972
	225	15	28	42	55	70	84	98	112	126	140	154	168	182	196
9.	11.712	19.279	12.657	12.233	14.044	11.957	14.442	11.246	14.044	12.940	14.966	12.762	20.038	12.769	14.213
	194	102	103	117	131	225	219	9	23	36	50	64	78	92	106
10.	21.854	13.232	13.798	14.598	13.750	15.282	12.555	15.270	14.376	12.662	11.468	15.047	11.458	13.231	9.520
	165	179	193	207	221	10	21	33	52	66	80	94	108	122	136
11.	15.715	14.496	14.691	9.565	13.568	15.619	20.468	15.683	12.158	14.329	11.892	13.049	14.443	14.672	15.311
	120	134	148	162	176	190	204	218	9	23	35	49	63	77	91
12.	15.320	14.565	13.447	13.672	12.163	13.543	17.124	15.430	11.541	15.761	12.541	12.572	13.005	14.503	13.211
	28	44	58	72	86	100	114	128	142	156	170	184	198	212	9
13.	13.595	14.072	14.721	13.625	15.159	15.026	14.547	11.255	15.248	17.167	12.198	14.849	13.567	14.712	22.520
	35	49	103	117	131	145	159	173	187	201	215	9	16	32	46
14.	13.130	13.593	13.995	13.831	13.949	13.986	15.040	15.170	15.162	15.025	15.531	17.707	13.055	13.951	13.621
	210	226	33	47	61	75	89	103	117	131	145	159	173	187	201
15.	14.898	15.010	15.935	15.167	14.586	13.930	15.271	15.072	14.643	15.077	15.637	11.292	14.127	15.346	14.348